

```

Db      235 KLEPSGPTSTINPCPECKCHKCPAPMLEGSPSEFIPPEIKDVLMLISLPKVCYVVDV 294
Qy      294 SHEDPEVKFMVYDGVENHAKTKPREOYNSTYRVSVLTVLHODMLNKEKCKSKNK 353
Db      295 SEDPDVQISMVFNNEVLTQOTOTREDYNSTIRVSLPIQODMMSKEFECKVNNK 354
Qy      354 ALPAPIEKTISKAKGPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQ 413
Db      355 DLPAPIERTISKIKGIYRAPQVYITLSPPEQLSKVDVSLCLAVGSPEDISVEMTISNGH 414
Qy      414 PENNYKTPPVYLDSDGSFFLYSKLTVDKSKMOGCVNFSCVMHDLNHNHYOKSLSPG 473
Db      415 TEENYKDTAPVLDSDGSFFLYSKLNMKTSKEMKTDSPSCVNRHGLKNYLYKTIISRSPG 474
Qy      474 K 474
Db      475 K 475

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RESULT 14
147159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: 147159
R:Kacskovics, I.; Sun, J.; Butler, J. E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: 147158; MUID:95015845; PMID:7930579
A:Accession: 147159
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:9433123; PIDD:AA52217.1; PID:9433124
A:Gene: IgG2a
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
F:133-202/Domain: Immunoglobulin homology <IMM>

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Query Match      50.4%; Score 1267; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 1.6e-66;
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;

Qy      145 ASTKGSPVPLAPSSKSTSGTAAGCLVLDYFPEPVTVSMNSGALTSGYHTPPAVLQSS 204
Db      1  APKTAFLVYPLAPCGRDTSGPNVALGCLASSYFPEPVTVWNSGALTSGYHTPPSVLQPS 60
Qy      205 GLYSLSSVTVVPSSSLGCTQYICNVNHPKPSNTKVKRVERPKSCDKHTPCPPCAPELLGG 264
Db      61  GLYSLSSMVTVPASSLSKSYTCNVNHPATTTKVKRKGKTRKPCPICPACESP---G 116
Qy      265 PSVFLEPPPKRDLMTSRPEVTCVVDVSHEDPEVKFNNYVGVGVENHNAKTKPREQYN 324
Db      117 PSVFLEPPPKRDLMTSRPOVTCVVDVSOENPEVOFSWYVGVENHTAQTRKEQOFN 176
Qy      325 STYRVSVLTVLHODMNLNGEKYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSREE 384
Db      177 STYRVSVLTPIQODMNLNGEKFCKVNNKDLPAPIITRIISKAKGQTERPOVYTLPPHAE 236
Qy      385 MTKNOVSLTCLVKGFYPSDIAVEMESNGQ--PENNYKTPPVYLDSDGSFFLYSKLTVDKS 442
Db      237 LSRKSVSITCLVIGFYPPDIDVEMQRNGQPEPEGNRYRTTPOQDVGDGYFLYSKFSYDKA 296
Qy      443 RMOGCVNFSCVMHDLNHNHYOKSLSPGK 474
Db      297 SWOGGIFQCAVMHDLNHNHYOKSLSPGK 328

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RESULT 15
147160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)

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```

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: 147160
R:Kacskovics, I.; Sun, J.; Butler, J. E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: 147158; MUID:95015845; PMID:7930579
A:Accession: 147160
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:9433125; PIDD:AA5218.1; PID:9433126
A:Gene: IgG2b
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
F:133-202/Domain: Immunoglobulin homology <IMM>

```

```

Query Match      50.2%; Score 1261; DB 2; Length 328;
Best Local Similarity 69.6%; Pred. No. 3.5e-66;
Matches 231; Conservative 41; Mismatches 54; Indels 6; Gaps 2;

Qy      145 ASTKGSPVPLAPSSKSTSGTAAGCLVLDYFPEPVTVSMNSGALTSGYHTPPAVLQSS 204
Db      1  APKTAFLVYPLAPCGRDTSGPNVALGCLASSYFPEPVTVWNSGALTSGYHTPPSVLQPS 60
Qy      205 GLYSLSSVTVVPSSSLGCTQYICNVNHPKPSNTKVKRVERPKSCDKHTPCPPCAPELLGG 264
Db      61  GLYSLSSMVTVPASSLSKSYTCNVNHPATTTKVKRKGKTRKPCPICPACESP---G 116
Qy      265 PSVFLEPPPKRDLMTSRPEVTCVVDVSHEDPEVKFNNYVGVGVENHNAKTKPREQYN 324
Db      117 PSVFLEPPPKRDLMTSRPOVTCVVDVSOENPEVOFSWYVGVENHTAQTRKEQOFN 176
Qy      325 STYRVSVLTVLHODMNLNGEKYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSREE 384
Db      177 STYRVSVLTPIQODMNLNGEKFCKVNNKDLPAPIITRIISKAKGQTERPOVYTLPPHAE 236
Qy      385 MTKNOVSLTCLVKGFYPSDIAVEMESNGQ--PENNYKTPPVYLDSDGSFFLYSKLTVDKS 442
Db      237 LSRKSVSITCLVIGFYPPDIDVEMQRNGQPEPEGNRYRTTPOQDVGDGYFLYSKFSYDKA 296
Qy      443 RMOGCVNFSCVMHDLNHNHYOKSLSPGK 474
Db      297 SWOGGIFQCAVMHDLNHNHYOKSLSPGK 328

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Search completed: September 12, 2003, 13:04:25
 Job time : 37.4831 secs

[illegible]

Db 61 GGGLEMGVYINPNKDGTRKFNKFKGKATLTISDKSSNAYMELSLTSEDSAVVYCAADYD 120

Qy 121 VTMTVLVNGGFWDGQGT RVTVSSASTKGPBVPFLADSKSTSGTALACLVKDYFPEP 180

Db 121 YDM-----FAVYGQGTLYTVSSAAKTKTPPSVYPLAAGCGDITGSSVTSCGLVKGYPES 173

Qy 181 VTVSMNAGALTSYHTFPRAVLQSSGLYSLSVTVVPSSSLGTORYTICNVHKKPSNTKVDK 240

Db 174 VTVSMNAGSLSSSVHTLQSGALQGLTVMSSSVTVPSSTMPSQVTVTSVAHAPASSTVVDK 233

Qy 241 RVEPKSCDKT-HTCP-----CPAPELLGSPVFLPPKPKDMLTMRPEVYCVVDV 293

Db 234 KLEPSGPISTINPCRPCKECHKCPAPNLEGSPSFIPTPNKDKVLMISLTIPKTYCVVDV 293

Qy 294 SHEDPEVAKFNNYVDGVEVHNNAKTKPREQYNSTYRVVSVLTVLHQDLNKEPKYCKVSNK 353

Db 294 SEDPDVQVISMFNANVEHTAQOTQHREDYNSTIRVYSTLPIQHDMWMSKEFKCKVNNK 353

Qy 354 ALPAPIETKTSKAGQPREPOVYTLTPPSREEMTINQVSLTCLVKGFTPSDIAVMEWENQ 413

Db 354 DLPSPERTKTSKIGLVRAAPQVYLLPPAPDLSEKRDVSLCLVGFNPGDISVEMWISNGH 413

Qy 414 PENNYKTPPVLVDGDSGSPFLSKTLVYVKSROQGNVPSCSVMHEALNNHTOKSLSLSPG 473

Db 414 TEENYKTPVPLVDSDGSTFIYSKLNKMTSKMEKIDTDFSCVNRHGLNRYLTKITISNPG 473

Qy 474 K 474

Db 474 K 474

RESULT 13

S01321

Ig gamma-2b chain precursor - mouse

C.Species: Mus musculus (house mouse)

C.Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999

C.Accession: S01321

Ride Waelle, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fliers, W.

Eur. J. Biochem. 176, 287-295, 1988

A.Title: Expression in non-T-lymphoid cells of mouse recombinant immunoglobulin directed

A.Reference number: S01320; MUID:88329081; PMID:318116

A.Accession: S01321

A.Molecule type: mRNA

A.Residues: 1-475

A.Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781

A.Note: This sequence was determined from the differentiated gene

C.Superfamily: Immunoglobulin C region; Immunoglobulin homology

C.Keywords: Immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:1-475/Product: Ig gamma-2b chain #status predicted <MAT>

F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 1401.5; DB 2; Length 475;

Best Local Similarity 55.3%; Pred. No. 3.8e-74;

Matches 266; Conservative 82; Mismatches 120; Indels 13; Gaps 4;

Qy 1 MEFGLSMFLVAIIKGVQCEVQLLESGGGLVQPGSLRLSCAASGFTFSNVAWSWYFOAP 60

Db 1 MEMTMIWFLFLISGTAGVQSQVQLQDSGAELARPAASVKLSCKASGYTLTSGISWVQRT 60

Qy 61 GKGLEWVASIASGSHSTYLAADSVKGRFTISRDNSKNTLYIQMNSLRADETAVYYCAKDRE 120

Db 61 GGGLEMGVYINPNKDGTRKFNKFKGKATLTISDKSSNAYMELSLTSEDSAVVYCAADYD 120

Qy 121 VTMVLVNGGFWDGQGT RVTVSSASTKGPBVPFLADSKSTSGTALACLVKDYFPEP 180

Db 121 YDM-----FAVYGQGTLYTVSSAAKTKTPPSVYPLAAGCGDITGSSVTSCGLVKGYPES 173

Qy 181 VTVSMNAGALTSYHTFPRAVLQSSGLYSLSVTVVPSSSLGTORYTICNVHKKPSNTKVDK 240

Db 174 VTVSMNAGSLSSSVHTLQSGALQGLTVMSSSVTVPSSTMPSQVTVTSVAHAPASSTVVDK 233

Qy 241 RVEPKSCDKT-HTCP-----CPAPELLGSPVFLPPKPKDMLTMRPEVYCVVDV 293

Db 234 KLEPSGPISTINPCRPCKECHKCPAPNLEGSPSFIPTPNKDKVLMISLTIPKTYCVVDV 293

Qy 294 SHEDPEVAKFNNYVDGVEVHNNAKTKPREQYNSTYRVVSVLTVLHQDLNKEPKYCKVSNK 353

Db 294 SEDPDVQVISMFNANVEHTAQOTQHREDYNSTIRVYSTLPIQHDMWMSKEFKCKVNNK 353

Qy 354 ALPAPIETKTSKAGQPREPOVYTLTPPSREEMTINQVSLTCLVKGFTPSDIAVMEWENQ 413

Db 354 DLPSPERTKTSKIGLVRAAPQVYLLPPAPDLSEKRDVSLCLVGFNPGDISVEMWISNGH 413

Qy 414 PENNYKTPPVLVDGDSGSPFLSKTLVYVKSROQGNVPSCSVMHEALNNHTOKSLSLSPG 473

Db 414 TEENYKTPVPLVDSDGSTFIYSKLNKMTSKMEKIDTDFSCVNRHGLNRYLTKITISNPG 473

Qy 474 K 474

Db 474 K 474

241 RVEPKSCDKT-HTCP-----CPAPELLGSPVFLPPKPKDMLTMRPEVYCVVDV 293

181 VTVSMNAGALTSYHTFPRAVLQSSGLYSLSVTVVPSSSLGTORYTICNVHKKPSNTKVDK 240

176 VTVSMNAGSLSSSVHTFPALIQ-SGLYTMSSSYTVPSSTMPSQVTVTSVAHAPASSTVVDK 234

241 RVEPKSCDKT-HTCP-----CPAPELLGSPVFLPPKPKDMLTMRPEVYCVVDV 293

Query Match	59.6%	Score 1498	DB 2	Length 470
Best Local Similarity	62.1%	Fred. No. 9.6e-80		
Matches 292	Conservative 61	Mismatches 107	Indels 10	Gaps 7
QY	8	LFVAILLGYOCCEVQLLESGGGILYOPGSGLSLSCAASGFTFSNMYAMSWAROAPGKGLDMV	67	
DB	8	LFVLSAPICGLISQVQLRSGSPSLVPSQGLTSLTCTGVSLSVYALTWVQAQKALELMV	67	
QY	68	SAISASGISTVLADSVKGRFTISDNKSNKITLYLQMSLRADPTAIYYCAKDREYMIYVL	127	
DB	68	GGIT-SSGTTIYNNPLKRLSLITENKSNQVLSLVSYVPEDTATYYCAR--KYYGEG	123	
QY	128	NGGF-DYVGQSTRVYSSASTKGPSVFPLAASSKTSKSGTAAIGCLIVDYEPPEYVSMN	186	
DB	124	DGAILADAGGGLVLTWSSASTTAPKRVYPLSSCCGDKSSSTYITGLGVSSMPEPTVWNN	183	
QY	187	SGALTSGVHTFPAYLQSSGLTSLSSVYTVPPSSLCTQYICNVNHNKPSNTKVDKRVKRS	246	
DB	184	SGALSGVHTFPAYLQSSGLTSLSSMVTVPPESTGS-QFTFNVAHPASTKVDKAVD-T	241	
QY	247	CDKHTTCCPCEAPELLGGSPVFLPPPKDPLTMSIRTEPVCVYVDVSHEDPEVKFMYV	306	
DB	242	C-KRSPCCCCCPPELPGSPVFIIPPKKDKTLITISGTEYVCVYVDVGHDEPEVKSMFV	300	
QY	307	DGVEYHNAKTIPREEQVNSTRYVSVTLVLHODMLNGEYCKCYKNKALPAPIETKISKA	366	
DB	301	DDVEYNTATTPRQEQFNSTRYVSALRIQHDMDGGEKFEKCYKNELPAPIVTTISRT	360	
QY	367	KGQRPQVYTLPREREEMTKNOVSLTLYVGFYSDSLAVEMESGG--ENNYTTPPV	424	
DB	361	KGPARQVYTLAPQDELSTKSYSLTQMYSFYDYLAVEMQRNGQFESEDKYTTTPPQ	420	
QY	425	LDSGSGFLYSLKLVYDKSRMOQGNVSCSVNHEALHNHYTOKSLSLSGK	474	
DB	421	LDASSYSLKLVYDKRNSMQEGDTLYCVNHEALHNHYTOKSTSKSGK	470	

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RESULT 8
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Duncancl, F.F.D
Submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49866.1; PID:g406253
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:276-345/Domain: Immunoglobulin homology <IM>

Query Match          59.0%; Score 1482.5; DB 2; Length 469;
Best Local Similarity 59.0%; Pred No. 7.6e-79;
Matches 281; Conservative 78; Mismatches 104; Indels 13; Gaps 7.

OY      4 GLSW-LRLVALKGVCEVOLLSEGGGLVDPGGSILRLSCAASGFPSFNAMSVNRQAPG 61
        ||| ||||| : |||:: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       2 GMSWIFLLSGTAGVHCIOQLQGSPELVRPGASVKISCAASGYTFDYIINWKQRPG 61
        ||| ||||| : |||:: ||| ||| ||| ||| ||| ||| ||| ||| |||

OY      62 KGLEVNSAI-SASGHSTLADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCAKDRE 120
        ||| :: | ||| : : || : : | : | : | : | : | : | : | : | : | :
Db       62 QGLRWIGIYPAASGNTRY-NENFGKATLTVDTSSTAYMOLSLTSDPTAVYFCARMG 120
        ||| :: | ||| : : || : : | : | : | : | : | : | : | : | : | :

OY      121 VTMIVLVNGEFDYMOCGRVTVSSASTKPSVEPLAPASKSNSGTALAGCIYKRPPEP 180
        | : : ||||| ||||| | ||| ||||| : : : ||||| |||||
Db       121 ATALL-----DYMGCGTLTYVSSAKTTAPSVYPLAPPCGDTGSVTLLGCLVKGYFEPP 175
        ||| :: | ||| : : || : : | : | : | : | : | : | : | : | : | :

OY      181 VTWSNMGALTSGVHTFPVLQSSGLYSLSVTVPSSSLCTQTYYICNVNHKPSNTKYDK 240
        ||| :: | ||| : : || : : | : | : | : | : | : | : | : | : | :

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Db	176	VLTITNNGSLSISCVNHFRAVLQSD-LYLTSSSVYUITSSTWPSQSLTCMAHNPASTYVK	234
Qy	241	RVEPKSCDHTNCRP--CPARELLGGPSVLEPRPKKDTLMSITREYTCVVDVSHEDP	298
Db	235	KIERPRG-PTIKPCRPCKAPMLLGGSPFIEPRKIKDVLISPLATCCVVDVSEDDP	293
Qy	299	EYKFNKYLQVGVENKAKTKRKREEDQNSNYRAYVSYLTVDHOMLNGKEKCKVSKALPAP	358
Db	294	DVQISWVNNVEKNTAQOTGNREDNLSLTRVYSLAPLQNDQMSGKEKCKVNNKQDLPAP	353
Qy	359	IEKTIKAKGQRPREDYUUTLPSPREEMTKNOVSLTCLGKGFPSDIAVEMESNGPERNNY	418
Db	354	IERETISKPGSVARQVUULPRPREEMTKKQVTLTLCWTDDEMPDIDYEVMTNNGKTELNY	413
Qy	419	KTPRPVLDSDGSFSLSKLTVDKSKMOGNNPSCSVMEALNNITYOKSLSLSPGK	474
Db	414	KNEPRVLDSDGSFSLSKLTVDKSKMVEENNSYSCVMEGALNNHTTKSSPRFGK	469

[illegible]

Query Match 65.1%; Score 1637.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred No. 6.2e-88;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 145 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLOSS 204
|||||
Db 1 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLOSS 60

QY 205 GLYSLSSVYTVSSSLGQTYICNVNHNKSNKTVKRV----- 242
|||||
Db 61 GLYSLSSVYTVSSSLGQTYICNVNHNKSNKTVKRVKRLKPLGLDTTTCRCRCPKSC 120

QY 243 -----EPKSCDTHKCPCPAPPELLGSGFVFLFPPKPKPT 277
|||||
Db 121 DTPPCPRCPREKSCDTPPCRCRCPKSCDTPPCRCRCPAPPELLGSGFVFLFPPKPKPT 180

QY 278 LMSRTPPEVTCVVDVSHEDPEVKFMVYDGVVHNAAKTPREEDQNSTFRVSVLTVLH 337
|||||
Db 181 LMSRTPPEVTCVVDVSHEDPEVKFMVYDGVVHNAAKTPREEDQNSTFRVSVLTVLH 240

QY 338 ODLWGKCKKCKVSKKALPAPTEKTSKAKGPREQVYTLPPSRPEMKNQVSLTCLVK 397
|||||
Db 241 ODLWGKCKKCKVSKKALPAPTEKTSKAKGPREQVYTLPPSRPEMKNQVSLTCLVK 300

QY 398 GFPPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMOGNYFSCSVME 457
|||||
Db 301 GFPPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMOGNYFSCSVME 360

QY 458 ALHNHYTOKSLSLSPGK 474
|||||
Db 361 ALHNHYTOKSLSLSPGK 377

RESULT 4
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence.revision 13-Jun-1983 #text_change 21-Jul-2000
A:Accession: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <EL>
A:Cross-References: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:96066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A:Reference number: A92809; MUID:81007673; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: Protein
A:Residues: 1-19, 'O', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Z1e
A:Accession: A90752
A:Molecule type: Protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Note: This sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Z1e
A:Accession: A93132

A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned

R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-References: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) and two heavy (H) chains. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 2.1e-86;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 145 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLOSS 204
|||||
Db 1 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLOSS 60

QY 205 GLYSLSSVYTVSSSLGQTYICNVNHNKSNKTVKRVKRLKPLGLDTTTCRCRCPKSC 264
|||||
Db 61 GLYSLSSVYTVSSSLGQTYICNVNHNKSNKTVKRVKRLKPLGLDTTTCRCRCPKSC 116

QY 265 PSYFLFPPKPKDTLMSRTPPEVTCVVDVSHEDPEVKFMVYDGVVHNAAKTPREEDQYN 324
|||||
Db 117 PSYFLFPPKPKDTLMSRTPPEVTCVVDVSHEDPEVKFMVYDGVVHNAAKTPREEDQYN 176

QY 325 STYRVYVTVTVHODLNKCKKCKVSKKALPAPTEKTSKAKGPREQVYTLPPSRREE 384
|||||
Db 177 STYRVYVTVTVHODLNKCKKCKVSKKALPAPTEKTSKAKGPREQVYTLPPSRREE 236

QY 385 MTKNOVSLTCLVKGFPPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 444
|||||
Db 237 MTKNOVSLTCLVKGFPPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 296

QY 445 OOGNPFVSCVMEALHNHYTOKSLSLSPGK 474
|||||
Db 297 OOGNPFVSCVMEALHNHYTOKSLSLSPGK 326

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence.revision 02-Apr-1982 #text_change 16-Jul-1999
A:Accession: A90933; A90249; A02150
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662

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RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match      65.2%; Score 1639.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 4.7e-88;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

OY      145  ASTGSPVFPPLAPSKSTSGGTALGCLVKDYPPEPVTVSYNSGALTSGVHTFPAVLQSS 204
Db      1  ASTGSPVFPPLAPSKSTSGGTALGCLVKDYPPEPVTVSYNSGALTSGVHTFPAVLQSS 60
OY      205  GLYSLSSVTVTPSSSLGTQTYICNVNHRKPSMTKYDKRV----- 242
Db      61  GLYSLSSVTVTPSSSLGTQTYICNVNHRKPSMTKYDKRVEL.TPLGDTHTTCRCDEPKSC 120
OY      243  -----EPKSCKTHTCRCPR.LPELLGSPVFLFPKPKDT 277
Db      121  DTPPPCRPCPEPKSCDTPPPRCPCPEPKSCDTPPPRCPR.LPELLGSPVFLFPKPKDT 180
OY      278  LMSRTPPEVTCVVVDVSHEDPEVKFNNYVSDGEVHNAAKTKI.REEDQNSTYRVSVLTLYLH 337
Db      181  LMSRTPPEVTCVVVDVSHEDPEVQFKMYVDGEVHNAAKTKI.REEDQNSTYRVSVLTLYLH 240
OY      338  QDWLNGKEYKKVKVSNKKALPAPIETKISAKQRPREPOYTT.PPSREKTKAQVSLTCLVK 397
Db      241  QDWLNGKEYKKVKVSNKKALPAPIETKISAKQRPREPOYTT.PPSREKTKAQVSLTCLVK 300
OY      398  GFYSDDIADVEENSGEOENNYKTTTPVLDSDGSFELYSKLI.VDKSRRMOQGVFCSVMHE 457
Db      301  GFYSDDIADVEENSGEOENNYKTTTPVLDSDGSFELYSKLI.VDKSRRMOQGNIFCSVMHE 360
OY      458  ALHNHYTKQKLSLSPGK 474
Db      361  ALHNRYTKQKLSLSPGK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:57:09 ; Search time 35.4831 seconds
(without alignments)
1284.668 Million cell updates/sec

Title: US-09-848-832-3

Perfect score: 2514

Sequence: 1 MEFGLSMFLVAILKGYOCE.....MHEALHNHYTKSLSPGK 474

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.9	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.2	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1610	64.0	326	1 G2HU	Ig gamma-4 chain C
5	1599.5	63.6	327	1 G4HU	Ig gamma-4 chain C
6	1527.5	60.8	444	2 PC4436	monoclonal antibody
7	1498	59.6	470	2 S22080	Ig heavy chain pre
8	1482.5	59.0	469	2 S37483	Ig gamma-2a chain
9	1455	57.9	472	2 S31459	Ig gamma-1 chain -
10	1442	57.4	374	2 S69339	Ig heavy chain V r
11	1429	56.8	446	2 S40295	Ig gamma-2a chain
12	1417	56.4	474	1 G2MS11	Ig gamma-2b chain
13	1401.5	55.7	475	2 S01321	Ig gamma-2b chain
14	1367	50.4	328	2 I47159	Ig gamma-2a chain
15	1361	50.2	328	2 I47160	Ig gamma-2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.5	234	2 PT0207	Ig gamma-1 chain C
18	1235	49.1	328	2 I47158	Ig gamma-1 chain C
19	1231.5	49.0	323	1 GHRB	Ig gamma chain C r
20	1231	49.0	328	2 I47161	Ig gamma-3 chain C
21	1210.5	48.2	329	2 G2GP	Ig gamma-2 chain C
22	1165.5	46.4	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3HWT	Ig gamma-3 heavy C
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3WSM	Ig gamma-3 chain C

30	1129	44.9	330	1 G2MSA	Ig gamma-2a chain
31	1127.5	44.8	329	2 S00847	Ig gamma-2c chain
32	1126.5	44.8	335	1 G2MSAB	Ig gamma-2a chain
33	1124	44.7	399	1 G2MSAM	Ig gamma-2a chain
34	1115	44.4	322	2 PS0019	Ig gamma-2a chain
35	1113	44.3	548	2 S38864	Ig epsilon chain C
36	1093.5	43.5	327	2 S06611	Ig gamma-2 chain C
37	1080	43.0	405	1 G2MSBM	Ig gamma-2 chain C
38	1070	42.6	277	2 I47162	Ig gamma-4 chain C
39	1003.5	39.9	249	2 S69340	Ig heavy chain VHI
40	879.5	35.0	572	2 B46529	Ig heavy chain (
41	868.5	34.5	549	2 S04845	Ig heavy chain pre
42	848	33.7	218	2 A36040	Ig heavy chain V-I
43	827	32.9	220	2 A49444	Ig gamma-1 heavy C
44	791.5	31.5	241	2 S69131	Ig heavy chain (D
45	791	31.5	627	2 S14683	Ig mu chain precu

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #ext_change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <BL>

A:Cross-references: EMBL:217370

A:Note: This sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) marker

A:Note: Lys-330 is removed after translation

R:Harits, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:217370

R:Rakhashli, N.; Ueda, S.; Obata, M.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943; PMID:681139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113:235-330 <TRK>

A:Cross-references: EMBL:217370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <GUN>

A:Note: this sequence has the Gln(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hirschmann, N.

Hope-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1


```

Db      61  ERLEWVASISVCG-TTYYPDMSKGRFTISRDNARNILYLQSLSLSESDTAMYYCCGFAD 119
QY      121  VMIVIVLNGCFDWMGGCTRTVTSASTKGRSVFPLAPSSKSTSGTALACLVKDYFPEP 180
Db      120  -----AMDYWGCGTLVTSSASTKGRSVFPLAPSSKSTSGTALACLVKDYFPEP 170
QY      181  VVVSNSGALTSGVHFPFPAVLQSSGLYSSSVTVTPSSSLGTQTYICNVNHRKPSNTRKVDK 240
Db      171  VVVSNSGALTSGVHFPFPAVLQSSGLYSSSVTVTPSSSLGTQTYICNVNHRKPSNTRKVDK 230
QY      241  RVEPKSCDTHTCPCPAPPELLGSPVFLFPPKPKDTLMISRPEVTCVVVDVSHEDPEV 300
Db      231  RVEPKSCDTHTCPCPAPPELLGSPVFLFPPKPKDTLMISRPEVTCVVVDVSHEDPEV 290
QY      301  KFMWYDGVENVNAKTRPREEOYNSTRVAVSVTLVHODMLNGEKYCKVSNKALPAPTE 360
Db      291  KFMWYDGVENVNAKTRPREEOYNSTRVAVSVTLVHODMLNGEKYCKVSNKALPAPTE 350
QY      361  KTISKAKGPREPOVYTLPPSRREEMTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYYKT 420
Db      351  KTISKAKGPREPOVYTLPPSRREEMTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYYKT 410
QY      421  TTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 474
Db      411  TTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 464

RESULT 15
ABP58273
ID  ABP58273 standard; Protein; 449 AA.
XX
AC  ABP58273;
XX
DT  31-MAR-2003 (first entry)
XX
DE  Humanised 3D6 antibody heavy chain.
XX
KW  Monoclonal antibody; 3D6; complementarity determining region; CDR;
KW  mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW  Down's syndrome; cerebral amyloid angiopathy; neuroprotective;
KW  nootropic.
XX
OS  Chimeric - Mus sp.
OS  Chimeric - Homo sapiens.
XX
FH  Key
FH  Region 1..119 Location/Qualifiers
FT  Region /note= "heavy chain variable region"
FT  Region 31..35 /note= "CDR1"
FT  Region 50..66 /note= "CDR2"
FT  Region 99..108 /note= "CDR3"
XX
XX  WO200288306-A2.
XX
XX  PD 07-NOV-2002.
XX
XX  PF 26-APR-2002; 2002WO-US11853.
XX
XX  PR 30-APR-2001; 2001US-287539P.
XX
XX  PA (ELIL ) LILLY & CO ELI.
XX
XX  PI Tsurushita N, Vasquez M;
XX
XX  DR MPI; 2003-183835/18.
XX
XX  PT New humanised forms of mouse 3D6 antibodies, useful for treating Down's
XX  syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
XX  amyloid angiopathy, or for inhibiting formation of or reducing Abeta

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PT  plaque in the brain -
XX
PS  Claim 5; Page 10-11; 54pp; English.
XX
CC  The present sequence is that of a preferred heavy chain of a
CC  humanised antibody of the present invention. In the variable region
CC  of this sequence, the complementarity determining regions (CDRs)
CC  originate from murine monoclonal antibody 3D6 and the framework region
CC  originates from human germline VH segment DP-45 and J segment JH4.
CC  Novel humanised antibodies of the invention have CDRs from 3D6 and
CC  human framework sequences. These humanised antibodies have binding
CC  affinities (affinity and epitope location) approximately the same
CC  as those of the mouse 3D6 antibody. The invention includes
CC  antibodies, single chain antibodies, and their fragments, as well
CC  as nucleotide sequences, vectors, transformed host cells, and
CC  methods of using the humanised antibody to treat, prevent,
CC  alleviate, reverse or otherwise ameliorate symptoms and/or
CC  pathology associated with Down's syndrome, (pre-)clinical
CC  Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy,
CC  and to inhibit formation or reduce Abeta plaque in the brain.
XX
SQ  Sequence 449 AA:
XX
Query Match 89.1%; Score 2241; DB 24; Length 449;
Best Local Similarity 92.3%; Pred. No. 3,7e-132;
Matches 420; Conservative 14; Mismatches 15; Indels 6; Gaps 1;

QY  20  EVOLLSEGGGLVDPGSLRLSCAASGFTSNVMSVROAPKGLGEWVASIASGHTYL 79
Db  1  EVOLVESGGGLVDPGSLRLSCAASGFTSNVMSVROAPKGLGEWVASIRGGGRITYY 60
QY  80  ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYCAKREVMIVVLNGFPDWGQGR 139
Db  61  SDNVKGRFTISRDNKNTLYLQNSLRAEDTAVYVVRDH-----YGGSDPYWGQGITL 114
QY  140  VTVSSASTKGPVFPPLAPSSKSTSGTALACLVKDYFPEPVTVSNSGALTSGVHTFPA 199
Db  115  VTVSSASTKGPVFPPLAPSSKSTSGTALACLVKDYFPEPVTVSNSGALTSGVHTFPA 174
QY  200  VLQSSGLYSSSVTVTPSSSLGTQTYICNVNHRKPSNTRKVDKREPKSCDTHTCPCPAP 259
Db  175  VLQSSGLYSSSVTVTPSSSLGTQTYICNVNHRKPSNTRKVDKREPKSCDTHTCPCPAP 234
QY  260  ELLGSPVFLFPPKPKDTLMISRPEVTCVVVDVSHEDPEVKFMWYDGVENVNAKTRPR 319
Db  235  ELLGSPVFLFPPKPKDTLMISRPEVTCVVVDVSHEDPEVKFMWYDGVENVNAKTRPR 294
QY  320  EEOYNSTRVAVSVTLVHODMLNGEKYCKVSNKALPAPLEKTIKSAKQPREPOVYTLPP 379
Db  295  EEOYNSTRVAVSVTLVHODMLNGEKYCKVSNKALPAPLEKTIKSAKQPREPOVYTLPP 354
QY  380  PSREEMTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYYKTTPVLDSDGSFFLYSKLTV 439
Db  355  PSREDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYYKTTPVLDSDGSFFLYSKLTV 414
QY  440  DKSRMQGNVFCSCVMHEALHNHYTKSLSPGK 474
Db  415  DKSRMQGNVFCSCVMHEALHNHYTKSLSPGK 449

Search completed: September 12, 2003, 13:00:39
Job time : 83.0085 secs

```

XX New antibodies that interact with osteoprotegerin ligands, useful for
PT treating osteoporotic disorders, e.g. osteoporosis, bone loss from
PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia
PT and osteonecrosis -
XX
PS Claim 1; Fig 2; 144pp; English.
XX
CC The invention relates to antibodies that interact with osteoprotegerin
CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in
CC a biological sample. The antibody, or the pharmaceutical composition
CC comprising the antibody, is also useful for treating osteoporotic disorder,
CC an inflammatory condition with attendant bone loss, an autoimmune
CC condition with attendant bone loss in a patient or rheumatoid arthritis
CC in a patient. In particular, the antibody or composition is useful for
CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,
CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria,
CC Menkes' syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or
CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
CC heavy chain.
XX
SQ Sequence 467 AA:
Query Match 89.3%; Score 2244.5; DB 24; Length 467;
Best Local Similarity 90.5%; Pred. No. 2.3e-132;
Matches 429; Conservative 14; Mismatches 24; Indels 7; Gaps 3;
QY 1 MEFGLSWLFLVAILIKGVQCEVQLLESGGLVDPGSLRLSCAASGFFPSNYAMSWVQAP 60
DB 1 MEFGLSWLFLVAILIKGVQCEVQLLESGGLVDPGSLRLSCAASGFFPSNYAMSWVQAP 60
QY 61 GKGLWWSAISASGSHSTYLDVSKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKDRE 120
DB 61 GKGLWWSAISASGSHSTYLDVSKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKDRE 120
QY 121 VTMLVNLNGGFYDVGQSTRTVSSASTKSPVPLAPSSKSTSGGTALGLVDPYPER 180
DB 121 VTMLVNLNGGFYDVGQSTRTVSSASTKSPVPLAPSSKSTSGGTALGLVDPYPER 180
QY 121 TTYIM--SWFDDPMAGGTLYTVSSASATKSPVPLAPSSKSTSGGTALGLVDPYPER 177
DB 121 TTYIM--SWFDDPMAGGTLYTVSSASATKSPVPLAPSSKSTSGGTALGLVDPYPER 177
QY 181 VTYSNNGALTSVGHTRPVALQSSGLYSLSVTVPSSTIGTQYTCNNHKKSNNTVYDK 240
DB 178 VTYSNNGALTSVGHTRPVALQSSGLYSLSVTVPSSTIGTQYTCNNHKKSNNTVYDK 237
QY 241 RVEKSCDKTHTCPCPAPRLGSPVFLPPPKKDTLMSRPPEVCYVVDVSHEDPEV 300
DB 238 TVERKCCVE---CPPCAPR-VACPSVFLPPPKKDTLMSRPPEVCYVVDVSHEDPEV 293
QY 301 KFMWYDGVENHNAKTRPREQYNSTYRVVSVLTVTHQDMLNGEKYCKVSNKALPAPIE 360
DB 294 OFNMWYDGVENHNAKTRPREQYNSTYRVVSVLTVTHQDMLNGEKYCKVSNKALPAPIE 353
QY 361 KITSKAGQRPQRYVTLPPSRREMTKNQVSLTCLVAGFSPSDIAVWESNGQPENNYKT 420
DB 354 KITSKTKGQRPQRYVTLPPSRREMTKNQVSLTCLVAGFSPSDIAVWESNGQPENNYKT 413
QY 421 TPPLVLDGSEFFLYSKTLVDKSRMQGNVSCSYMHALLNHYTKSLSPGK 474
DB 414 TPPLVLDGSEFFLYSKTLVDKSRMQGNVSCSYMHALLNHYTKSLSPGK 467

RESULT 14
AAR24812
ID AAR24812 standard; Protein; 466 AA.
XX
AC AAR24812;
XX
DT 25-MAR-2003 (updated)
DT 28-DEC-1992 (first entry)
XX
DE Sequence encoded by the chimeric H chain cDNA contained in pPB1373.
XX
KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;

KW antithrombotic agent; myocardial infarction therapy.
XX
OS Synthetic.
XX
FH Key
FT Peptide
FT 13..19
FT /label= Leader
FT 20..134
FT /label= VH
FT 135..232
FT /label= CH1
FT 233..247
FT /label= hinge
FT 248..357
FT /label= CH2
FT 358..464
FT /label= CH3
FT Misc-difference
FT /note= "translated stop codon"
FT
XX
PN EP491351-A2.
XX
PD 24-JUN-1992.
XX
PF 17-DEC-1991; 91BP-0121591.
XX
PR 18-DEC-1990; 90JP-00413829.
PR 11-NOV-1991; 91JP-0294464.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Iwasa S, Taka H, Watanabe T, Tada H;
XX
XX WPI. 1992-209528/26.
XX
DR N-PSDB; AAQ23692.
XX
PT Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
XX
PS Example; Figure 11; 87pp; English.
XX
XX plasmid pTB1373 contains the whole length of a mouse-human
CC chimeric anti-human fibrin heavy chain cDNA open reading
CC frame. It was prep. using Poly(A)+ RNA from the anti-fibrin
CC chimeric Ab-producing transformant FIB1-HOI/X63 as a template
CC to clone human C-Xappa cDNA, using the oligo-dT (pharmacia) primer as
CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'C1H
CC respectively as a primer for first strand cDNA synthesis and the
CC primer combination of 5'C1H and 3'C2H, of 5'EH and 3'C1H and of
CC 5'EH and 3'EH respectively as primers for PCR. The amplified gene
CC products were isolated and used to produce plasmids. After
CC confirmation of the cDNA sequence of each plasmid, the cDNA
CC encoding LH VH CH1 and CH2CH3 were joined together to give
CC plasmid pTB1373 contg. the whole length chimeric H chain
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-F1H,
CC (updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 466 AA:
Query Match 89.3%; Score 2244; DB 13; Length 466;
Best Local Similarity 90.5%; Pred. No. 2.5e-132;
Matches 424; Conservative 18; Mismatches 22; Indels 10; Gaps 2;
QY 1 MEFGLSWLFLVAILIKGVQCEVQLLESGGLVDPGSLRLSCAASGFFPSNYAMSWVQAP 60
DB 1 MDSRLNLVFLVLIILIKGVQCEVQLLESGGLVDPGSLRLSCAASGFFPSNYAMSWVQAP 60
QY 61 GKGLWWSAISASGSHSTYLDVSKGRTISRDNKNTLYLQMSLRAEDTAVYYCAKDRE 120

AAE33522
 ID AAE33522 standard; Protein; 447 AA.
 XX AAE33522;
 AC AAE33522;
 XX
 DT 02-APR-2003 (first entry)
 XX
 XX Human AQC2 heavy chain protein.
 DE
 XX Human; very late activation antigen; VLA-1; beta1 containing integrin;
 KM immunological disorder; inflammatory disorder; skin related condition;
 KM psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KM fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KM fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KM irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KM atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;
 KM gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KM osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KM systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KM renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KM hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KM graft versus host disease; myocardial ischaemia.
 XX
 XX Homo sapiens.
 OS
 XX WO200283854-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 12-APR-2002; 2002WO-US11521.
 PF
 XX 13-APR-2001; 2001US-283794P.
 PR 06-JUL-2001; 2001US-303689P.
 XX
 XX (BIOI) BIOGEN INC.
 PA
 XX Lyne PD, Garber EA, Saldanha JW, Karpusas M;
 XX WPI: 2003-093009/08.
 DR
 XX
 XX New anti-VLA-1 antibodies are useful for preventing or treating
 PT VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis,
 PT eczema, burns, dermatitis, and abnormal proliferation of hair follicle
 PT cells or fibrosis -
 XX
 XX
 PS Claim 6; Page 75; 248pp; English.
 CC The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; beta1 containing integrins) antigens and
 CC methods of using these antibodies to treat immunological disorders. The
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence
 CC is human AQC2 heavy chain protein.
 XX
 XX Sequence 447 AA:
 SQ
 Query Match 89.3%; Score 2244.5; DB 24; Length 447;
 Best Local Similarity 93.2%; Pred. No. 2.2e-132;

Matches 426; Conservative 6; Mismatches 12; Indels 13; Gaps 3;
 QY 20 EVQLVESGGGLVQPGGSLRLSCAASGFTTSNAMSVRAQPGKGLEWVAISAGHSITL 79
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTTSRYTMSVRAQPGKLEWVAITISGGH-YY 59
 QY 80 ADSVKGRFTISRDNKNTLYLQMNSSLRADDTAVYYCAK--DREVTMIIVLNGGFDYWGQ 136
 DB 60 LDSVKGRTISRDNKNTLYLQMNSSLRADDTAVYYCTRGFGD-----GGYFDYWGQ 110
 QY 137 GTRVTVSSASTKGPVSFPLAPSSKSTSGTALGCLVKDYFPEPVTVSNNSGALTSGVHT 196
 DB 111 GRLTVTVSSASTKGPVSFPLAPSSKSTSGTALGCLVKDYFPEPVTVSNNSGALTSGVHT 170
 QY 197 FRAVLQSSGLYSLSSVYTPSSSLGTQYTYICVNNKPSMTKYDKRREPSCDKTHTCPPC 256
 DB 171 FRAVLQSSGLYSLSSVYTPSSSLGTQYTYICVNNKPSMTKYDKRREPSCDKTHTCPPC 230
 QY 257 PAPELLGSPVFLPPPKPDITMISRTPEVTCVVVDVSHEDPEVKFMWYVDGEVHNMAKT 316
 DB 231 PAPELLGSPVFLPPPKPDITMISRTPEVTCVVVDVSHEDPEVKFMWYVDGEVHNMAKT 290
 QY 317 KPREQYNSTYRVYSVLTVLDHQMNLGKERYCKRKNKALPAPIETISKAKGQPREPOVY 376
 DB 291 KPREQYNSTYRVYSVLTVLDHQMNLGKERYCKRKNKALPAPIETISKAKGQPREPOVY 350
 QY 377 TLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPPVLDSCGFFLYSK 436
 DB 351 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSCGFFLYSK 410
 QY 437 LTVDKSRMQQGNVFSCSVMEALHNHYTQKSLSLSPG 473
 DB 411 LTVDKSRMQQGNVFSCSVMEALHNHYTQKSLSLSPG 447
 RESULT 13
 ABP71365
 ID ABP71365 standard; Protein; 467 AA.
 XX
 XX ABP71365;
 AC
 XX
 DT 28-APR-2003 (first entry)
 XX
 XX Anti-OPGL-1 antibody heavy chain.
 DE
 XX
 XX Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;
 KM antiarthritis; cyostatic; OPGL; anti-OPGL-1; antibody.
 KW
 XX Mus musculus.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /note= "Irg2 signal peptide"
 FT Region 20..141
 FT Region /note= "variable region"
 FT Region 142..467
 FT Region /note= "constant region"
 PN WO2003002713-A2.
 PD 09-JAN-2003.
 PF 25-JUN-2002; 2002WO-US20181.
 PR 26-JUN-2001; 2001US-301172P.
 PA (ABGE-) ABGENIX INC.
 PA (AMGE-) AMGEN INC.
 XX
 XX Boyle WJ, Martin FH, Corvalan JR, Davis GC;
 PI
 XX
 DR WPI: 2003-210262/20.
 DR N-PSDB; AB859147.

XX New chimeric T84.12 antibody active against carcinoembryonic
 PT antigen - has murine variable and human constant regions, also
 PT DNA encoding it and transformed myeloma cells

PS Claim 1: Page 22-23; 27pp; English.

XX The sequences (AA054651-52) show the light and heavy chain CDNA
 CC of murine T84.12. The T84.12 antibody is directed against the
 CC tumour marker carcinoma embryonic antigen, and is useful for
 CC tumour imaging and immunotherapy.

CC The amino acid sequence given in the specification has been
 CC incorrectly identified as a nucleic acid sequence, therefore
 CC unacceptable characters have been represented as an 'N'.
 CC The amino acid sequence given below has been derived from the
 CC cDNA, by the indexer.
 CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 477 AA;

Query Match 89.8%; Score 2257; DB 15; Length 477;
 Best Local Similarity 89.2%; Pred. No. 3.9e-133;
 Matches 423; Conservative 23; Mismatches 22; Indels 6; Gaps 2;

QY 1 MEFGLSWLEFVAILKGVQCEVQLLESGGLVOPGSLRLSCAASGFTFSNYAMSWVQAP 60
 DB 10 MNEFSLFLFLVYLKGVQCEVQLLESGGLVOPGSLRLSCAASGFTFSNYAMSWVQAP 69
 QY 61 GKGLEWYSAISAGSHSYTLADSVKGRFTISRDNSKNTLYLQMNSLRADTVAYTCARRE 120
 DB 70 EKRLEWVASISSDG-TFEYVDSVKGRFTVSRDNANKILYLQMSLSRSDTAMYYCAR--- 125
 QY 121 VTMIIVLNGGFDYMGQGTFRVTVSSASTKGPVFPFLAPSSKTSGGTALGCLVNDYFPEP 180
 DB 126 --IDYGGGGGYMGQGTALAVSAASTKGPVFPFLAPSSKTSGGTALGCLVNDYFPEP 183
 QY 181 VTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDK 240
 DB 184 VTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDK 243
 QY 241 RVEKSCDKHTPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDASHEDEV 300
 DB 244 KVEKSCDKHTPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDASHEDEV 303
 QY 301 KFNMYVDGVEVHNNAKTRREDOYNSTYRVSVLTFLVHODMLNGKEYCKVSNKALPAPIE 360
 DB 304 KFNMYVDGVEVHNNAKTRREDOYNSTYRVSVLTFLVHODMLNGKEYCKVSNKALPAPIE 363
 QY 361 KTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKT 420
 DB 364 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKT 423
 QY 421 TTPVLDSGGSFLLSKLTVDKSRMOQGNVFSCVMHEALHNHYTQKSLSLSPGK 474
 DB 424 TTPVLDSGGSFLLSKLTVDKSRMOQGNVFSCVMHEALHNHYTQKSLSLSPGK 477

RESULT 11
 AAE34876
 ID AAE34876 standard; Protein: 444 AA.
 AC AAE34876;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE B1WA4/8 antibody heavy chain mature protein.
 XX
 KW B1WA8 antibody; heavy chain variable region; light chain variable region;
 XX VH; VU; CD44v6; medicament; cancer; antibody therapy.
 OS Unidentified.
 XX
 PN WO200294879-A1.

XX 28-NOV-2002.
 PD
 XX
 PE 17-MAY-2002; 2002WO-EP05467.
 XX
 PR 18-MAY-2001; 2001EP-0112237.
 XX
 PR 26-SEP-2001; 2001US-325147P.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Adolf G, Ostermann E, Patzelt E, Spiroli M, Heijer K, Miglietta JU;
 PI Van Dongen AAMS;
 DR WPI: 2003-129413/12.
 DR N-PSDB: AAD53212, AAD53215.
 XX
 XX New antibodies specific for an epitope coded by the variant exon of the
 PT CD44 gene, useful for treating cancer, including non-small cell lung,
 PT breast, head and neck, ovarian and lung cancer
 PS Claim 24: Column 44; 78pp; English.

XX The present invention relates to novel antibody molecules comprising a
 CC variable region of the heavy (VH) and/or light chain (VL) of CD44v6
 CC specific humanised antibody called B1WA8 and B1WA4. Sequences of the
 CC invention are useful for manufacturing a medicament and for treating
 CC cancer including colorectum, non-small cell lung, breast, head and neck,
 CC ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the
 CC brain. They are also useful in antibody therapy. The present sequence
 CC is B1WA4/8 antibody heavy chain mature protein. This sequence is used
 CC in the exemplification of the invention.

XX Sequence 444 AA;

Query Match 89.5%; Score 2249.5; DB 24; Length 444;
 Best Local Similarity 92.7%; Pred. No. 1.1e-132;
 Matches 422; Conservative 12; Mismatches 10; Indels 11; Gaps 1;

QY 20 EVOLLESGGLVOPGSLRLSCAASGFTFSNYAMSWVQQAQKGLEWYSAISAGSHSYTL 79
 DB 1 EVOLLESGGLVOPGSLRLSCAASGFTFSNYAMSWVQQAQKGLEWYSAISAGSHSYTL 60
 QY 80 ADSVKGRTISRDNKNTLYLQMNSLRADTVAYTCARREYTMIVLNGGFDYMGQGT 139
 DB 61 LDSIKGRTISRDNKNTLYLQMNSLRADTVAYTCARREYTMIVLNGGFDYMGQGT 109
 QY 140 VTVSSASTKGPVFPFLAPSSKTSGGTALGCLVNDYFPEPVTVMNSGALTSGVHTFPA 199
 DB 110 VTVSSASTKGPVFPFLAPSSKTSGGTALGCLVNDYFPEPVTVMNSGALTSGVHTFPA 169
 QY 200 VLOSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDKRVERKSCDKHTPCPCAP 259
 DB 170 VLOSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDKRVERKSCDKHTPCPCAP 229
 QY 260 ELLEGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNMYVDGVEVHNNAKTRPR 319
 DB 230 ELLEGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNMYVDGVEVHNNAKTRPR 289
 QY 290 EEQYNSTYRVSVLTFLVHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 349
 DB 320 EEQYNSTYRVSVLTFLVHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379
 QY 380 PSREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTPVLDSGGSFLLSKLTV 439
 DB 350 PSREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTPVLDSGGSFLLSKLTV 409
 QY 440 DKSRMOQGNVFSCVMHEALHNHYTQKSLSLSPGK 474
 DB 410 DKSRMOQGNVFSCVMHEALHNHYTQKSLSLSPGK 444

RESULT 12

[illegible]

KW CD3 antigen-T-cell receptor complex; graft rejection; cancer.
XX Synthetic.
OS Rattus sp.
OS Homo sapiens.
XX MO200005268-A1.
XX
XX 03-FEB-2000.
XX
XX 21-JUL-1999; 99WO-GB02380.
XX
XX 21-JUL-1998; 98GB-0015909.
XX
XX (B7G1-) B7G INT LTD.
XX
XX Waldmann H, Frewin M;
XX WPI: 2000-182655/16.
XX N-PSDB: AAZ60599.
XX
XX New humanized anti-CD3 antibodies, used for treating cancer or for
XX immunosuppression and preventing graft rejection
XX
XX Disclosure; Page 45-47; 56pp; English.
XX
XX The present sequence represents the heavy chain variable region of a rat
XX immunoglobulin G (IgG) antibody which is specific for the CD3 antigen
XX complex, and the human CH1-hinge-anti-lycosylCH2CH3. The specification
XX describes chimeric human/rodent anti-CD3 antibodies, which have a
XX rodent CD3 light chain variable region and a human heavy chain variable
XX region. The anti-CD3 antibodies can render T-cells non-functional by
XX antibody blockade of the CD3 antigen-T-cell receptor (TCR) complex.
XX They can be used for immunosuppression, particularly for the control
XX of graft rejection. The antibodies can also enhance or re-direct T-cell
XX responses to antigens. They can be used in the treatment of cancer.
XX
XX Sequence 449 AA;

Query Match 90.7%; Score 2279; DB 21; Length 449;
Best Local Similarity 94.5%; Pred. No. 1.5e-134;
Matches 430; Conservative 8; Mismatches 11; Indels 6; Gaps 1;
QY 20 EVOLLESGGGLVOPGSLRLSCAASGFTFSNYAMSWRQAPGKLEWVSAISAGHSTYL 79
DB 1 EVOLLESGGGLVOPGSLRLSCAASGFTFSNYAMSWRQAPGKLEWVSTISGGRITTY 60
QY 80 ADSVKGRTISRDNKNTLYIQMNSLRADTAAYVYCAKDREVTMIIVLNGSGFDYWGQCTR 139
DB 61 RDSVKGRTISRDNKNTLYIQMNSLRADTAAYVYCAKFRQ-----YSGGFDYWGQCTL 114
QY 140 VTVSSASTKGPSPVPLAPSSKSTSGTAAAGCLVKIYDPPEPVTVSWNSGALTSGVHPFPA 199
DB 115 VTVSSASTKGPSPVPLAPSSKSTSGTAAAGCLVKIYDPPEPVTVSWNSGALTSGVHPFPA 174
QY 200 VLAGSGLYSLSSVYTVVSSSLGDTQYICNVNHNKPSNTRKVDKRVKPSKCDKTHTPPCAP 259
DB 175 VLAGSGLYSLSSVYTVVSSSLGDTQYICNVNHNKPSNTRKVDKRVKPSKCDKTHTPPCAP 234
QY 260 ELLEGPSVFLFPPPKPTLMSRTPPEVTCVVVDVSHEDPEVKFMYVVDGVEVHNAAKTPR 319
DB 235 ELLEGPSVFLFPPPKPTLMSRTPPEVTCVVVDVSHEDPEVKFMYVVDGVEVHNAAKTPR 294
QY 320 EEOVNSTYRVVSVLTVLDHOMLNGEKVKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLR 379
DB 295 EEOVNSTYRVVSVLTVLDHOMLNGEKVKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLR 354
QY 380 PSREMTKNOVSLTCLVKGFTPSDIAVEMESNGOPENNYKTTTPYLDSDGSFFLYSKLTV 439
DB 355 PSREMTKNOVSLTCLVKGFTPSDIAVEMESNGOPENNYKTTTPYLDSDGSFFLYSKLTV 414
QY 440 DKSRWQGNVFSQVMHEALHNHYTOKSLSLSPGK 474

DB 415 DKSRWQGNVFSQVMHEALHNHYTOKSLSLSPGK 449
RESULT 8
AAEI2715
ID AAEI2715 standard; Protein; 451 AA.
XX
XX AAEI2715;
XX
XX 04-JAN-2002 (first entry)
XX
XX Human recombinant immunoglobulin (Ig) heavy chain region.
XX
XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX heavy chain region; cancer; breast; ovary; lung; bladder;
XX cytostatic; therapy; immunoglobulin; Ig.
XX
XX Homo sapiens.
XX
XX MO200175110-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10589.
XX
XX 30-MAR-2000; 2000US-0538913.
XX
XX (DYAX-) DYAX CORP.
XX
XX Hoogenboom HRJM, Henderikx MPG;
XX
XX WPI: 2001-626437/72.
XX N-PSDB: AAD20745.
XX
XX Novel isolated tumor-associated antigen mucin-1-specific binding member
XX for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX its portion for binding to an epitope of the protein core of mucin-1
XX
XX Claim 12; Page 106-108; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
XX (MUC-1)-specific binding member comprising an antigen binding domain
XX region having an antibody variable light (VL) or heavy (VH) region,
XX or a complementarily determining region (CDR) of VL or VH. MUC1-specific
XX binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX The binding of MUC1-specific binding member to MUC1 is detected by a
XX detection method selected from enzyme-linked immunosorbent assay,
XX magnetic resonance imaging, scintillation counting, and X-ray film.
XX MUC1-specific binding member is useful for treating cancer, preferably
XX adenocarcinoma, in an individual, where the cancer is present in tissue
XX of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX binding member is useful for diagnosing and imaging MUC1-expressing
XX cancer cells and tissues, for purifying or isolating non-glycosylated,
XX underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX containing molecules, and for therapeutically or prophylactically
XX treating cancer. The present sequence is human recombinant immunoglobulin
XX (Ig) heavy chain region (variable VH and CH constant heavy chain).
XX
XX Sequence 451 AA;
SO
Query Match 89.8%; Score 2257; DB 22; Length 451;
Best Local Similarity 93.2%; Pred. No. 3.7e-133;
Matches 428; Conservative 7; Mismatches 12; Indels 12; Gaps 2;
QY 20 EVOLLESGGGLVOPGSLRLSCAASGFTFSNYAMSWRQAPGKLEWVSAISAGHSTYL 79
DB 1 QVOLVOSGGGLVOPGSLRLSCAASGFTFSNANAGWRQAPGKLEWVSGISGSGSTYY 60
QY 80 ADSVKGRTISRDNKNTLYIQMNSLRADTAAYVYCAKDREVTMIIVLNGS----PYWG 135
DB 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAAYVYCAK-----TGGGVWMPIDYWG 112
QY 136 QGTRVTVSSASTKGPSPVPLAPSSKSTSGTAAAGCLVKIYDPPEPVTVSWNSGALTSGVH 195

[illegible]

RESULT 6	
AAU07745	
ID	AAU07745 standard; Protein; 461 AA.
XX	
AC	
AAU07745;	
XX	
DT	04-DEC-2001 (first entry)
XX	
DE	Humanised monoclonal antibody Hu266, heavy chain.
XX	
KM	Monoclonal antibody; Hu266; neurotropic; neuroprotective; Abeta peptide.
KM	Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
KM	gene therapy.
XX	
OS	Mus sp.
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FH	Peptide
FT	Location/Qualifiers
FT	1..19
FT	/label= Signal_peptide
FT	Protein
FT	20..461
FT	/label= Mature_Hu266_heavy_chain
FT	/note= "This sequence is specifically claimed in
FT	claim 17"
XX	
PN	WO200162801-A2.
XX	
PD	30-AUG-2001.
XX	
PF	26-FEB-2001; 2001WO-US06191.
XX	
ER	24-FEB-2000; 2000US-0184601.
PR	08-DEC-2000; 2000US-0254465.
PR	08-DEC-2000; 2000US-0254498.
XX	
PA	(UNITED) UNIV WASHINGTON.
PA	(ELIL) LILLY & CO ELI.
XX	
I1	Holtzman DM, Demattos R, Bales KR, Paul SM, Tsunashita N;

PI	Vasquez M.
XX	
DR	WP1; 2001-550087/61.
XX	
PT	New humanised antibody for the treatment of Alzheimer's comprises the
PT	inhibition and reduction of the formation of amyloid plaques -
PS	
XX	Example 13; Fig 5; 63pp: English.
XX	
CC	The invention relates a humanised antibody that specifically binds
CC	an epitope contained within positions 13-28 of amyloid beta peptide,
CC	Abeta. The antibody is useful to inhibit and reduce the formation of
CC	amyloid plaques or the effects of toxic soluble Abeta species in humans
CC	their fragments are used for the manufacture of a medicament. This includes
CC	the prolonged expression of recombinant sequences of them in human
CC	tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
CC	Down's syndrome or pre clinical cerebral amyloid angiopathy.
CC	Specifically, the antibody is used to sequester Abeta into plasma, brain
CC	or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
CC	peptide within the brain thereby improving cognition. The present
CC	sequence is the heavy chain of a humanised monoclonal antibody, Hu266,
CC	based on the mouse antibody 266.
XX	
SQ	Sequence 461 AA:
	Query Match 91.7%; Score 2304.5; DB 22; Length 461;
	Best Local Similarity 91.8%; Pred. No. 4,1e-136;
	Matches 435; Conservative 13; Mismatches 13; Indels 13; Gaps 1
OY	1.MEFGSLMFLVAIIKVGCEVOYLESGGGLVPGGSLRLSCAASGFTFSNYMSWRQP 60
DB	1.MNFGSLTFLVLVLYLKGVCEVOLVESGGGLVPGGSLRLSCAASGFTFSYMSWRQP 60
OY	61.GKGLEWVAISASGHSTYLADSVKGRFTISRDNSSNTLYLQNSSLRAEDTAAYCAKDRE 120
DB	61.GKGLELVAINQSIVGNSTYYPTDVKGRFTISRDNANTLYLQNMSLRAEDTAAYYCASG-- 118
OY	121.VTMIVLVNGDFDWOGSTRVTVSSASTKGPVSFPLAPSSKTSGGTAALGCLVKDYFPKP 180
DB	119-----DYMGOGLTVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPKP 167
OY	181.VTVSNNSGALNSGVTFFPAVLIOSSLLYSLSVVYPSSSLGTQTYICNNHNPSTKKYDK 240
DB	168.VTVSNNSGALNSGVTFFPAVLIOSSLLYSLSVVYPSSSLGTQTYICNNHNPSTKKYDK 227
OY	241.RVEPKSGCKTHTCPCPCPAPPELLIGGSVLFEPKPKADTLIMSTRPEVCVYVDSHPDEY 300
DB	228.KVEPKSCKHTCPCPCPAPPELLIGGSVLEFPKPKADTLIMSTRPEVCYVVDVSHDDPEY 287
OY	301.KFNMYVDDEVENNAKTCPREEQYNSTYRVSVLTVALHDMDLNGKEKCKVSKNALPAPIE 360
DB	288.KFNMYVDDEVENNAKTCPREEQYNSTYRVSVLTVALHDMDLNGKEKCKVSKNALPAPIE 347
OY	361.KTISKAKQPREPOVYTLPSPSRERETKNQVSLITCLVKGFPESDIAVEWESNQPENNYKT 420
DB	348.KTISKAKQPREPOVYTLPSPSRDELTKNQVSLITCLVKGFPESDIAVEWESNQPENNYKT 407
OY	421.TRPVLDSDGSFFLYSKLTVNDKSRMQOQNVFCSVMHEALHNHYTQKSISLSPGK 474
DB	408.TRPVLDSDGSFFLYSKLTVNDKS RMQOQNVFCSVMHEALHNHYTQKSISLSPGK 461
RESULT 7	
AAy68810	
XX	AAy68810 standard; Protein; 449 AA.
XX	
AC	AAy68810;
XX	
DT	16-MAY-2000 (first entry)
XX	
DE	A rat heavy chain region and a human hinge region.
XX	
KX	CD3 antigen complex; chimeric antibody; immunosuppression; heavy chain;

PN WO20028306-A2.
 XX 07-NOV-2002.
 PD
 XX
 XX 26-APR-2002; 2002MO-US11853.
 PF
 XX 30-APR-2001; 2001US-287539P.
 PR
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Tsunushita N, Vasquez M;
 PI
 XX
 XX WPI; 2003-183835/18.
 DR N-PSDB; AB224633, AB224635.
 XX
 PT New humanized forms of mouse 3D6 antibodies, useful for treating Down's
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
 PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta
 PT plaque in the brain -
 XX
 XX
 PS Disclosure; Page 13-14; 54pp; English.
 CC The present sequence is that of a preferred heavy chain of a
 CC humanised antibody of the present invention. In the variable
 CC region of this sequence, the complementarity determining regions
 CC (CDRs) originate from murine monoclonal antibody 3D6 and the
 CC framework region from human germline VH segment DP-45 and J segment
 CC JH4. Novel humanised antibodies of the invention have CDRs from 3D6
 CC and human framework sequences. These humanised antibodies have
 CC binding affinities (affinity and epitope location) approximately the
 CC same as those of the mouse 3D6 antibody. The invention includes the
 CC antibodies, single chain antibodies, and their fragments, as well
 CC as nucleotide sequences, vectors, transformed host cells, and
 CC methods of using the humanised antibody to treat, prevent,
 CC alleviate, reverse or otherwise ameliorate symptoms and/or
 CC pathology associated with Down's syndrome, (pre-)clinical
 CC Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy,
 CC and to inhibit formation or reduce Abeta plaque in the brain.
 CC
 XX
 XX Sequence 468 AA:
 SQ

Query Match 92.18; Score 2315; DB 24; Length 468;
 Best Local Similarity 91.68; Pred. No. 9.1e-137;
 Matches 434; Conservative 16; Mismatches 18; Indels 6; Gaps 1;

QY 1 MEGGLSWLFLVALKQVCEVOLLSEGGGLVQPGSGRLSCAASGFTFSNYAMSWAQAP 60
 DB 1 MNGFLSLIFLVALKGVQCEVOLVESGGGLVQPGSGRLSCAASGFTFSNYGMSWROAP 60
 QY 61 GKGLIEWNSAISAGSHSTYLADSVKGRFTISRDNKSKNTLYQNMNLSRAEDPAVYCAKDRE 120
 DB 61 GKGLIEWNSAISRSGGRTYYDYNKGRFTISRENAKNSLYQNMNLSRAEDPAVYCAVYDH 120
 QY 121 VTMIIVNLNGEDYWGQTRVTVSSASTKGPVFLAPSSKSTSGTAAALCLVXDYFPEP 180
 DB 121 -----YSGGSDYWGQGLTVTVSSASTKGPVFLAPSSKSTSGTAAALCLVXDYFPEP 174
 QY 181 VTWSMNSGALTSGVHPPAVLQSSGLYSVTVTPSSSLGTQTYICNNVHKRSNRYDK 240
 DB 175 VTWSMNSGALTSVGHPPAVLQSSGLYSVTVTPSSSLGTQTYICNNVHKRSNRYDK 234
 QY 241 RVEPKSGDKTHTPCPCAPAPRLGSPSYFLRPPKPKDTLMTSRPEVYCVVVDVSHEDPEV 300
 DB 235 KVEPKSGDKTHTPCPCAPAPRLGSPSYFLRPPKPKDTLMTSRPEVYCVVVDVSHEDPEV 294
 QY 301 KFMWYVDGVEVNAKTKPREDOYNSTYRVVSVLTVLHODMLNCKEYCKVSNKALPAPIE 360
 DB 295 KFMWYVDGVEVNAKTKPREDOYNSTYRVVSVLTVLHODMLNCKEYCKVSNKALPAPIE 354
 QY 361 KTSKAKGQREPOVYTLPPSRDEMTKNOVSLTCLVKGFPDIAVEMESNGPENNYKT 420
 DB 355 KTSKAKGQREPOVYTLPPSRDELTKNVSLTCLVKGFPDIAVEMESNGPENNYKT 414

QY 421 TPVYLDSDGSFFLYSKLTVDKSRWQGNVFSQSVYMHAEALHNEYTOKSLSPCK 474
 DB 415 TPVYLDSDGSFFLYSKLTVDKSRWQGNVFSQSVYMHAEALHNEYTOKSLSPCK 468

RESULT 5
 ID AAR20057
 AC AAR20057;
 AC AAR20057;
 DT 25-MAR-1992 (first entry)
 XX
 XX Heavy chain of 3D6 anti-HIV antibody.
 DE
 XX Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;
 KW complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal
 FT Region 20..49
 FT /label= Framework_1
 FT Region 50..54
 FT /label= CDR-1
 FT Region 55..68
 FT /label= Framework_2
 FT Region 69..85
 FT /label= CDR_2
 FT Region 86..117
 FT /label= Framework_3
 FT Region 118..134
 FT /label= CDR_3
 FT Region 135..145
 FT /label= Framework_4
 FT Region 146..475
 FT /label= Constant_region
 XX
 XX WO9118983-A.
 PN
 XX 12-DEC-1991.
 PD
 XX 28-MAY-1991; 91MO-1000067.
 PF
 XX 29-MAY-1990; 90AT-0001178.
 PR
 XX (JUNG/) JUNGBAUER A.
 PA
 XX Feigenhauer M, Himmeler G, Kohl J, Steindl F;
 PI
 XX WPI; 1992-007468/01.
 DR N-PSDB; AAQ20066.
 DR
 PT Recombinant protein which binds to complex viral antigen and
 PT HIV-1 - contains variable region of antibody derived from 3D6
 PT cell line, used for detecting HIV-1 antigen
 PT
 XX
 XX Claim 2; Page 24; 52pp; German.
 PS
 XX The variable region of the heavy chain is used in a recombinant
 CC protein with the variable region from the kappa light chain of 3D6,
 CC the two V regions being joined by a linker. The recombinant protein
 CC binds to HIV gp160.
 CC See also AAQ20067 and AAQ20068.
 CC
 XX
 XX Sequence 475 AA:
 SQ

Query Match 91.98; Score 2309.5; DB 13; Length 475;
 Best Local Similarity 91.48; Pred. No. 2e-136;
 Matches 438; Conservative 13; Mismatches 19; Indels 9; Gaps 2;

OY 421 TPPLVLDSDGSFFLYSKLTVDKSRMOOGNFFSCSYMHEALHNHYTOKSLSPGK 474
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 TPPLVLDSDGSFFLYSKLTVDKSRMOOGNFFSCSYMHEALHNHYTOKSLSPGK 474

RESULT 3
 AAU14288 standard; Protein: 477 AA.

AC AAU14288;

DT 24-OCT-2001 (first entry)

DE Human novel protein #159.

XX Human; novel protein. Antianaemic; osteopathic; antinflammatory;
 KW Immunomodulatory; cytoskeletal; neuroprotective; vulnereary; nootropic;
 KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
 KW pharmacolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.

OS Homo sapiens.

PN MO200155437-A2.

XX 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02623.

PR 25-JAN-2000; 2000US-0491404.

XX (HSE-) HSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI: 2001-451939/48.

DR N-PSDB: AAS22593.

PT Isolated polypeptides useful for treating anti-inflammatory diseases,
 XX nervous system disorders, and for regenerating bone and cartilage -

PS Example 4: Page 611-612; 894pp: English.

CC The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicite an immune response, to determine quantitatively
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.

XX Sequence 477 AA:

Query Match 93.5%; Score 2351.5; DB 22; Length 477;
 Best Local Similarity 92.7%; Pred. No. 4,9e-139;
 Matches 442; Conservative 13; Mismatches 19; Indels 3; Gaps 1;

OY 1 MEEGLSMFLVALILKGVCEVOLLEBSGGGLVOPGSGLRISCAAGFTFSNVMWVRQAP 60
 Db 1 MEEGLSMFLVALILKGVCEVOLLEBSGGGVOPGRSLRISCAAGFTFSNVMHWVRQAP 60
 OY 61 GKLEWVAIAIWYDGSKRKYADSVKGFRTISRNSKNTLYLQNNSLRAEDTAYVYCAKDR- 119
 Db 61 GKLEWVAIAIWYDGSKRKYADSVKGFRTISRNSKNTLYLQNNSLRAEDTAYVYCAKDR 120
 OY 120 --EVTMIVLNGCFDVGQGTFRVTWSASTKGPVFPPLAPSSKSTSGTAAAGCLVKDFE 177
 Db 121 WYRTYTTVTITGYFPDWGQGLTVTVYSSASTKGPVFPPLAPSSKSTSGTAAAGCLVKDFE 180
 OY 178 PEPVTVSNMNGALTSQVHTFPAVLQSSGLYSVVTVVPSSSLGTQTYICNVNHRPSNPK 237
 Db 181 PEPVTVSNMNGALTSQVHTFPAVLQSSGLYSVVTVVPSSSLGTQTYICNVNHRPSNPK 240
 OY 238 VDKRVEPKSCDTHTCPPCPAPBELLGSPVFLFPPKPKPTLMISTRPEYTCVVVDVSHED 297
 Db 241 VDKRVEPKSCDTHTCPPCPAPBELLGSPVFLFPPKPKPTLMISTRPEYTCVVVDVSHED 300
 OY 298 PEYKFMWYDGYEVHNAKTPPREEOYNSTRVSVLTJLHOMLNGKEYCKVSNKALPA 357
 Db 301 PEYKFMWYDGYEVHNAKTPPREEOYNSTRVSVLTJLHOMLNGKEYCKVSNKALPA 360
 OY 358 PIEKTSKAKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEMWSNQPENN 417
 Db 361 PIEKTSKAKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEMWSNQPENN 420
 OY 418 YKTTTPVLDSDGSFFLYSKLTVDKSRMOOGNFFSCSYMHEALHNHYTOKSLSPGK 474
 Db 421 YKTTTPVLDSDGSFFLYSKLTVDKSRMOOGNFFSCSYMHEALHNHYTOKSLSPGK 477

RESULT 4
 ABP58275
 ID ABP58275 standard; Protein: 468 AA.

AC ABP58275;

DT 31-MAR-2003 (first entry)

DE Humanised 3D6 antibody heavy chain.

XX Monoclonal antibody; 3D6; complementarity determining region; CDR;

KW mouse; human; humanised antibody; antibody; Alzheimer's disease;

KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective;

XX nootropic.

OS Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Signal_peptide

FT /label= Mature_peptide

FT /note= "the mature heavy chain is claimed in Claim 5"

FT Region 20..138

FT /note= "heavy chain variable region, claimed in Claim 4"

FT Region 50..54

FT /note= "CDR1"

FT Region 69..85

FT /note= "CDR2"

FT Region 118..127

FT /note= "CDR3"

PT useful for treating individual exposed to rabies virus and for
 PT preventing spread of rabies virus to central nervous system -
 PS Claim 4; Page 23-24; 25pp; English.

CC This sequence represents the heavy chain protein of the monoclonal
 CC antibody from clone JA. The invention relates to an isolated human
 CC monoclonal rabies virus neutralising antibody (vitrucide) derived from
 CC cDNA clones encoding the antibody heavy and light chains expressed in
 CC heterologous expression systems and purified away from deleterious
 CC contaminants. The invention provides a fused gene encoding a chimeric
 CC immunoglobulin light chain and a fused gene encoding a chimeric
 CC immunoglobulin heavy chain. The antibody of the invention is useful for
 CC treating an individual exposed to a rabies virus by administering to the
 CC individual a therapeutically effective amount of the antibody, and
 CC preventing a spread of the rabies virus to the central nervous system
 CC (CNS). The antibody of the invention provides a safe and efficacious post
 CC -exposure prophylactic therapy for individuals exposed to a rabies virus.

XX Sequence 474 AA;

Query Match 100.0%; Score 2514; DB 23; Length 474;
 Best Local Similarity 100.0%; Pred. No. 3,4e-149;
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFGLSMFLVAILKGVQCEVQLLESGGGLVQPGSLRLSCAAGFTFSNYAMSVROAP 60
 Db 1 MEFGLSMFLVAILKGVQCEVQLLESGGGLVQPGSLRLSCAAGFTFSNYAMSVROAP 60
 QY 61 GKLEWWSAISASGHSTYLADSVKGRFTISDNSKNTLYLQMSLRADTAIVYYCANDRE 120
 Db 61 GKLEWWSAISASGHSTYLADSVKGRFTISDNSKNTLYLQMSLRADTAIVYYCANDRE 120
 QY 121 VTMLVNLNGGFDYNGGRTYVSSASTKGPVFPFLAPSSKTSCTGTAALGCLVNDYPERP 180
 Db 121 VTMLVNLNGGFDYNGGRTYVSSASTKGPVFPFLAPSSKTSCTGTAALGCLVNDYPERP 180
 QY 181 VTMVNSGALTSVHTPPAVLQSSGLVSLSSVTPVPSSTLTQTYICNVNHRPSNTKYDK 240
 Db 181 VTMVNSGALTSVHTPPAVLQSSGLVSLSSVTPVPSSTLTQTYICNVNHRPSNTKYDK 240
 QY 241 RVEPKSCDKHTPCPCAPPELLGSPVFLPPPKRDTLMTSRTEVTCVVVDVSHEDPEV 300
 Db 241 RVEPKSCDKHTPCPCAPPELLGSPVFLPPPKRDTLMTSRTEVTCVVVDVSHEDPEV 300
 QY 301 KFNMYVDGVEVHNKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE 360
 Db 301 KFNMYVDGVEVHNKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE 360
 QY 361 KTISKAGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFTYPSDIAVEMESNGQDENNYKT 420
 Db 361 KTISKAGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFTYPSDIAVEMESNGQDENNYKT 420
 QY 421 TPVPLDSDGSFELYSKLTVDKSRMQQGVNFCVMEHLAHNHYTQKSLSPGK 474
 Db 421 TPVPLDSDGSFELYSKLTVDKSRMQQGVNFCVMEHLAHNHYTQKSLSPGK 474

RESULT 2

ABU08017 standard; Protein: 474 AA.

AC ABU08017;

DT 10-MAY-2003 (first entry)

DE Human monoclonal rabies virus antibody heavy chain, clone JH, protein.

XX Human; antibody; constant region; monoclonal antibody 57;

KW Mab 57; variable region; Rabies; neurological disease; infection;
 KW central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
 KW pathogen; vaccine; virucide; heavy chain.

XX

OS Homo sapiens.

XX W02003016501-A2.

XX 27-FEB-2003.

XX 21-AUG-2002; 2002WO-US26584.

XX 21-AUG-2001; 2001US-314023P.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Hooper DC, Dietzschold B;

XX WPI: 2003-276566/27.

XX N-PSDB: ABX12855.

PT New recombinant antibody comprising a constant region of Mab 57 linked
 PT to a non-Mab 57 variable region, useful for treating an individual
 PT exposed to a pathogen, e.g. rabies infection -

XX Example 1; Page 32-33; 38pp; English.

CC The invention discloses a recombinant antibody comprising a constant
 CC region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
 CC region. Rabies is an acute, neurological disease caused by infection of
 CC the central nervous system with the rabies virus, a member of the
 CC Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
 CC for producing a recombinant antibody by culturing a host cell,
 CC containing a recombinant expression vector comprising the nucleic acid
 CC molecule encoding the antibody, and isolating the recombinant antibody
 CC expressed and treating an individual exposed to a pathogen by
 CC administering to the individual the recombinant antibody. The recombinant
 CC antibodies are useful for preventing (vaccine) and treating an individual
 CC exposed to a pathogen, e.g. rabies infection. They are also useful for
 CC the qualitative and quantitative determination of the rabies virus. The
 CC sequences presented are the antibody protein fragments, the nucleic acids
 CC encoding them or the PCR primers used to construct the recombinant
 CC expression vector.

XX Sequence 474 AA;

Query Match 100.0%; Score 2514; DB 24; Length 474;
 Best Local Similarity 100.0%; Pred. No. 3,4e-149;
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFGLSMFLVAILKGVQCEVQLLESGGGLVQPGSLRLSCAAGFTFSNYAMSVROAP 60
 Db 1 MEFGLSMFLVAILKGVQCEVQLLESGGGLVQPGSLRLSCAAGFTFSNYAMSVROAP 60
 QY 61 GKLEWWSAISASGHSTYLADSVKGRFTISDNSKNTLYLQMSLRADTAIVYYCANDRE 120
 Db 61 GKLEWWSAISASGHSTYLADSVKGRFTISDNSKNTLYLQMSLRADTAIVYYCANDRE 120
 QY 121 VTMLVNLNGGFDYNGGRTYVSSASTKGPVFPFLAPSSKTSCTGTAALGCLVNDYPERP 180
 Db 121 VTMLVNLNGGFDYNGGRTYVSSASTKGPVFPFLAPSSKTSCTGTAALGCLVNDYPERP 180
 QY 181 VTMVNSGALTSVHTPPAVLQSSGLVSLSSVTPVPSSTLTQTYICNVNHRPSNTKYDK 240
 Db 181 VTMVNSGALTSVHTPPAVLQSSGLVSLSSVTPVPSSTLTQTYICNVNHRPSNTKYDK 240
 QY 241 RVEPKSCDKHTPCPCAPPELLGSPVFLPPPKRDTLMTSRTEVTCVVVDVSHEDPEV 300
 Db 241 RVEPKSCDKHTPCPCAPPELLGSPVFLPPPKRDTLMTSRTEVTCVVVDVSHEDPEV 300
 QY 301 KFNMYVDGVEVHNKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE 360
 Db 301 KFNMYVDGVEVHNKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE 360
 QY 361 KTISKAGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFTYPSDIAVEMESNGQDENNYKT 420
 Db 361 KTISKAGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFTYPSDIAVEMESNGQDENNYKT 420

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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:46:18 ; Search time 81.0085 Seconds
(without alignments)
928.747 Million cell updates/sec

Title: US-09-848-832-3

Perfect score: 2514
Sequence: 1 MEEGLSWLFLVALILKGVCE.....MHEALHNHYTKSLSLSPGK 474

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2514	100.0	474	23	AA014065 Heavy chain protel
2	2514	100.0	474	24	ABU08017 Human monoclonal r
3	2351.5	93.5	477	22	AA014288 Human novel protel
4	2315	92.1	468	24	ABP58275 Humanised 3D6 anti
5	2309.5	91.9	475	13	AA020057 Heavy chain of 3D6
6	2304.5	91.7	461	22	AAU07745 Humanised monoclon
7	2279	90.7	449	21	AA568810 A rat heavy chain
8	2257	89.8	451	22	AAE12715 Human recombinant
9	2257	89.8	451	24	ABU58807 Mucin 1 (MUC-1) b1

10	2257	89.8	477	15	AA047453	Ch1784.12 H3 heavy
11	2249.5	89.5	444	24	AAE34876	B1M4/8 antibody h
12	2244.5	89.3	447	24	AAE33522	Human AOC2 heavy c
13	2244.5	89.3	467	24	ABP71365	Anti-OPGL-1 antibo
14	2244	89.3	466	13	AA024812	Sequence encoded b
15	2241	89.1	449	24	ABP58273	Humanised 3D6 anti
16	2238.5	89.0	447	24	AAE33523	Human AOC2 heavy c
17	2238	89.0	470	23	ABG77158	Germine protein s
18	2237.5	89.0	442	24	ABE80109	Heavy chain. Homo
19	2237.5	89.0	442	24	ABR39465	Humanised anti-Abe
20	2237.5	89.0	442	24	ABU08311	Humanised 266 anti
21	2235	88.9	468	23	ABU10365	Human breast speci
22	2234.5	88.9	447	24	AAE33524	Human AOC2 heavy c
23	2232.5	88.8	449	23	AA018400	Mature humanised m
24	2226.5	88.6	442	24	ABE80113	Deglycosylated hea
25	2226.5	88.6	442	24	ABR39474	Humanised anti-Abe
26	2226.5	88.6	442	24	ABU08320	Humanised antibody
27	2221.5	88.4	459	14	AA042066	Human anti-HBs hea
28	2221	88.3	464	23	ABG78151	Human antibody fra
29	2221	88.3	464	23	ABG91842	Human Fv molecule
30	2220	88.3	582	22	AAE81987	Ganglioside CD3 sp
31	2219	88.3	470	23	AAU81993	Amino acid sequenc
32	2218.5	88.2	519	23	AAU81993	Human secreted pro
33	2196	87.4	470	23	ABE81109	Anti-tissue factor
34	2196	87.4	470	23	ABP72748	Anti-tissue factor
35	2193.5	87.3	452	20	AA029458	Recombinant immuno
36	2193.5	87.3	452	21	AA030322	Humanised anti-IL-
37	2193.5	87.3	452	21	AA077766	Humanised anti-IL-
38	2193.5	87.3	452	24	ABU59512	Humanised Mouse an
39	2193.5	87.3	452	24	ABU13799	Humanised mouse an
40	2188	87.0	470	23	ABG77161	Amino acid sequenc
41	2187.5	87.0	473	23	ABG77162	Germine protein s
42	2187	87.0	476	23	ABE81110	Anti-VEGF heavy ch
43	2184.5	86.9	452	19	AA069316	Anti-IL-8 humanise
44	2183	86.8	478	19	AA063763	Macaque primatized
45	2183	86.8	478	23	AAU11644	Protein sequence o

ALIGNMENTS

RESULT 1	
AA014065	standard; Protein: 474 AA.
AC	AA014065:
XX	
XX	
DT	07-MAY-2002 (first entry)
XX	
DE	Heavy chain protein of the monoclonal antibody from clone JA.
XX	
KW	HRIG: human rabies-immune globulin; monoclonal; virucide; heavy chain;
KW	human monoclonal rabies virus neutralising antibody; immunoglobulin;
KW	light chain; central nervous system; CNS; prophylactic therapy; clone JA.
OS	
OS	Homo sapiens.
XX	
PN	WO200188132-A2.
XX	
PD	22-NOV-2001.
XX	
PF	04-MAY-2001; 2001WO-US14468.
XX	
PR	16-MAY-2000; 2000US-204518P.
XX	
XX	(UYJE-) UNIV JEFFERSON THOMAS.
PA	
PI	Hooper DC, Dietzschold B.
XX	
DR	WPI: 2002-062381/08.
XX	
PT	N-PSDB; AAK98701.
XX	
XX	Novel isolated human monoclonal rabies virus neutralising antibody

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OM protein - protein search, using sw model

Run on: September 12, 2003, 13:00:49 : Search time 15.2034 Seconds
(without alignments)
2245.783 Million cell updates/sec

Title: US-09-848-832-4

Perfect score: 1223

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Scoring table:

BLOSUM62

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Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	234	US-10-225-108A-4	Sequence 4, Appli
2	1223	100.0	234	US-09-848-832-4	Sequence 4, Appli
3	1108.5	99.6	235	US-10-153-382-7	Sequence 7, Appli
4	1096	89.6	233	US-10-153-382-15	Sequence 15, Appli
5	1085.5	88.8	234	US-10-153-382-11	Sequence 11, Appli
6	1076	88.0	236	US-09-859-053-34	Sequence 34, Appli
7	1066	87.2	236	US-09-859-053-38	Sequence 38, Appli
8	1057	86.4	224	US-09-453-234-82	Sequence 82, Appli
9	1057	86.4	224	US-09-453-234-88	Sequence 88, Appli
10	1054	86.4	224	US-09-453-234-90	Sequence 90, Appli
11	1054	86.4	224	US-09-453-234-36	Sequence 36, Appli
12	1045	85.4	224	US-09-453-234-84	Sequence 84, Appli
13	1043	85.3	224	US-09-453-234-46	Sequence 46, Appli
14	1027	84.0	238	US-10-216-484-107	Sequence 107, App
15	1015	83.0	236	US-09-859-053-30	Sequence 30, Appli

16	1015	83.0	238	US-10-216-484-50	Sequence 50, Appli
17	1009.5	82.5	241	US-10-221-945-1	Sequence 1, Appli
18	999	81.7	238	US-10-216-484-109	Sequence 109, App
19	997	81.5	238	US-10-216-484-129	Sequence 129, App
20	994	81.3	238	US-10-216-484-131	Sequence 131, App
21	993	81.2	234	US-09-740-002-24	Sequence 24, Appli
22	993	81.2	238	US-10-216-484-52	Sequence 52, Appli
23	993	81.2	238	US-10-216-484-127	Sequence 127, App
24	991	81.0	215	US-09-791-153A-47	Sequence 47, Appli
25	987	80.7	226	US-09-453-234-74	Sequence 74, Appli
26	986	80.6	212	US-10-006-593-118	Sequence 118, App
27	985	80.5	238	US-09-453-234-86	Sequence 86, Appli
28	985	80.5	238	US-10-216-484-54	Sequence 54, Appli
29	984.5	80.5	215	US-09-972-656-100	Sequence 100, App
30	983.5	80.5	239	US-09-249-011A-72	Sequence 22, Appli
31	982	80.3	226	US-09-453-234-50	Sequence 50, Appli
32	982	80.3	226	US-09-453-234-80	Sequence 80, Appli
33	982	80.3	240	US-10-159-006-36	Sequence 36, Appli
34	981.5	80.3	234	US-10-026-925-55	Sequence 55, Appli
35	980	80.1	226	US-09-453-234-38	Sequence 38, Appli
36	977	79.9	224	US-09-453-234-52	Sequence 52, Appli
37	976	79.8	226	US-09-453-234-42	Sequence 42, Appli
38	976	79.8	236	US-10-006-593-69	Sequence 69, Appli
39	975.5	79.8	213	US-10-150-475A-4	Sequence 44, Appli
40	973	79.6	224	US-09-453-234-44	Sequence 78, Appli
41	973	79.6	224	US-09-453-234-78	Sequence 40, Appli
42	972	79.5	224	US-09-453-234-40	Sequence 72, Appli
43	972	79.5	226	US-09-453-234-72	Sequence 38, Appli
44	970	79.3	238	US-10-171-452A-38	Sequence 56, Appli
45	970	79.3	238	US-10-171-452A-56	

ALIGNMENTS

RESULT 1					
US-10-225-108A-4					
Sequence 4, Application US/10225108A					
Publication No. US20030157112A1					
GENERAL INFORMATION:					
APPLICANT: HOOVER, Craig					
APPLICANT: DIETZSCHOLD, Bernhard					
TITLE OF INVENTION: Recombinant Antibodies, and Compositions					
TITLE OF INVENTION: and Methods for Making Them					
FILE REFERENCE: 8321-110					
CURRENT APPLICATION NUMBER: US/10/225,108A					
CURRENT FILING DATE: 2003-04-10					
PRIOR APPLICATION NUMBER: US 09/848, 832					
PRIOR FILING DATE: 2001-05-04					
PRIOR APPLICATION NUMBER: US 60/204,518					
PRIOR FILING DATE: 2001-05-16					
PRIOR APPLICATION NUMBER: US 60/314,023					
PRIOR FILING DATE: 2001-08-21					
NUMBER OF SEQ ID NOS: 16					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 4					
LENGTH: 234					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-10-225-108A-4					
Query Match					
Best Local Similarity 100.0%: Score 1223: DB 12, Length 234:					
Matches 234: Conservative 0: Mismatches 0: Indels 0: Gaps 0:					
QY	1 MEAPAQQLFLLLMLPDTTGGEIVLQSPFTLSPEPERA:ILACRASQTSRYLAWQCKP 60				
DB	1 MEAPAQQLFLLLMLPDTTGGEIVLQSPFTLSPEPERA:ILACRASQTSRYLAWQCKP 60				
QY	61 GQAPRLIYDTSNRATGIPARFSGSGGDFLTLSISLE:EDPFAVYCCQQRNWPVTFQO 120				
DB	61 GQAPRLIYDTSNRATGIPARFSGSGGDFLTLSISLE:EDPFAVYCCQQRNWPVTFQO 120				

Oy 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180
Db 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180
Oy 181 ESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC 234
Db 181 ESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC 234

RESULT 2

US-09-848-832-4
; Sequence 4, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
; FILE REFERENCE: H0001.NP0002
; CURRENT APPLICATION NUMBER: US/09/848, 832
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/204, 518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-832-4

Query Match 100.0%; Score 1223; DB 12; Length 234;
Best Local Similarity 100.0%; Pred. No. 1,2e-72;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MEAPAOQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
Db 1 MEAPAOQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
Oy 61 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSSLEPEDFAVYYCQQRFPNMPWTFGQ 120
Db 61 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSSLEPEDFAVYYCQQRFPNMPWTFGQ 120
Oy 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180
Db 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180
Oy 181 ESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC 234
Db 181 ESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC 234

RESULT 3

US-10-153-382-7
; Sequence 7, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PEIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153, 382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-7

Query Match 90.6%; Score 1108.5; DB 15; Length 235;

Best Local Similarity 91.5%; Pred. No. 3.5e-65;
Matches 215; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Oy 1 MEAPAOQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 59
Db 1 MEAPAOQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
Oy 60 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSSLEPEDFAVYYCQQRFPNMPWTFG 119
Db 60 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSSLEPEDFAVYYCQQRFPNMPWTFG 120
Oy 120 QGTKEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 179
Db 120 QGTKEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 180
Oy 180 QSVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC 234
Db 180 QSVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC 235

RESULT 4

US-10-153-382-15
; Sequence 15, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PEIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153, 382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-15

Query Match 89.6%; Score 1096; DB 15; Length 234;
Best Local Similarity 91.0%; Pred. No. 2.3e-64;
Matches 213; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Oy 1 MEAPAOQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
Db 1 MEAPAOQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
Oy 61 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSSLEPEDFAVYYCQQRFPNMPWTFGQ 120
Db 61 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSSLEPEDFAVYYCQQRFPNMPWTFGQ 120
Oy 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180
Db 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180
Oy 181 ESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC 234
Db 181 ESVTEODSKDSTYSLSTLTLSKADYEKHKYACEVTHOGLSSPVTKSFNRGEC 234

RESULT 5

US-10-153-382-11
; Sequence 11, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PEIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153, 382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23

NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-382-11

Query Match 88.8%; Score 1085.5; DB 15; Length 233;
Best Local Similarity 91.0%; Pred. No. 1.1e-63;
Matches 213; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQOK 60
DB 1 METPAQLLFLLMLPDTTGEIVLTQSPETLSLSPGERATLSCRNS-VSSSLYAWYQOKP 59
QY 61 GOAPRLLYDTSNRATGIPARFSGSGSTDFLTLSISLEPEDFAVYVCOQRFNMPWTFQ 120
DB 60 GOAPRLLYGASSRATGIPDRFSGSGSTDFLTLSISLEPEDFAVYVCOQYGISPTFGG 119
QY 121 GATKEFRRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVOMKVDNALQSGNSQ 180
DB 120 GATKEFRRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVOMKVDNALQSGNSQ 179
QY 181 ESVTEQDSKSDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234
DB 180 ESVTEQDSKSDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 6
US-09-859-053-34
Sequence 34, Application US/09859053
Patent No. US20020102658A1

GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859, 053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-34

Query Match 88.0%; Score 1076; DB 10; Length 236;
Best Local Similarity 90.3%; Pred. No. 4.6e-63;
Matches 213; Conservative 6; Mismatches 15; Indels 2; Gaps 2;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQOK 59
DB 1 METPAQLLFLLMLPDTTGEIVLTQSPETLSLSPGERATLSCRASQNTSRSSYLAWYQOK 60
QY 60 PCQARLLIYDTSNRATGIPARFSGSGSTDFLTLSISLEPEDFAVYVCOQRFNMPW-TF 118
DB 61 PCQARLLIYGASSRATGIPDRFSGSGSTDFLTLSISLEPEDFAVYVCOQYGISPTFGG 120
QY 119 GCGTVEFRRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVOMKVDNALQSGN 178
DB 121 GCGTVEFRRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVOMKVDNALQSGN 180
QY 179 SOESTVEDSKSDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234
DB 178 SOESTVEDSKSDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234

DB 181 SOESTVEDSKSDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 7
US-09-859-053-38
Sequence 38, Application US/09859053
Patent No. US20020102658A1

GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859, 053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-38

Query Match 87.2%; Score 1066; DB 10; Length 236;
Best Local Similarity 89.4%; Pred. No. 2e-62;
Matches 211; Conservative 9; Mismatches 14; Indels 2; Gaps 2;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQOK 59
DB 1 METPAQLLFLLMLPDTTGEIVLTQSPETLSLSPGERATLSCRASQNTSRSSYLAWYQOK 60
QY 60 PCQARLLIYDTSNRATGIPARFSGSGSTDFLTLSISLEPEDFAVYVCOQRFNMPW-TF 118
DB 61 PCQARLLIYGASSRATGIPDRFSGSGSTDFLTLSISLEPEDFAVYVCOQYGISPTFGG 120
QY 119 GCGTVEFRRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVOMKVDNALQSGN 178
DB 121 GCGTVEFRRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVOMKVDNALQSGN 180
QY 179 SOESTVEDSKSDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234
DB 181 SOESTVEDSKSDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 8
US-09-453-234-82
Sequence 82, Application US/09453234
Publication No. US20030091995A1

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkiers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453, 234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157, 415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 82
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens

OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match 86.4%; Score 1057; DB 11; Length 224;
Best Local Similarity 95.8%; Pred. No. 7.5e-62;
Matches 204; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 21 EIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKPGQAPRLLYDTSNRTGIPA 80
DB 1 EIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKPGQAPRLLYDTSNRTGIPA 60
QY 81 RFSGSGGTDTLTLSISLEPEDFAVYCCQQRPNMPTFGQGTKEFKRTVAAPSVFIIPP 140
DB 61 RFSGSGGTDTLTLSISLEPEDFAVYCCQQRPNMPTFGQGTKEFKRTVAAPSVFIIPP 120
QY 141 SDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYLSSTLT 200
DB 121 SDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYLSSTLT 180
QY 201 LSKADYEKHKYACEVTHQGLSSPYTKSFNRGE 233
DB 181 LSKADYEKHKYACEVTHQGLSSPYTKSFNRGE 213

RESULT 9
US-09-453-234-88

Sequence 88, Application US/09453234
Publication No. US20030091995A1

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453, 234
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157, 415
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 88
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-34L
US-09-453-234-88

Query Match 86.4%; Score 1057; DB 11; Length 224;
Best Local Similarity 95.8%; Pred. No. 7.5e-62;
Matches 204; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 21 EIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKPGQAPRLLYDTSNRTGIPA 80
DB 1 EIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKPGQAPRLLYDTSNRTGIPA 60
QY 81 RFSGSGGTDTLTLSISLEPEDFAVYCCQQRPNMPTFGQGTKEFKRTVAAPSVFIIPP 140
DB 61 RFSGSGGTDTLTLSISLEPEDFAVYCCQQRPNMPTFGQGTKEFKRTVAAPSVFIIPP 120
QY 141 SDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYLSSTLT 200
DB 121 SDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYLSSTLT 180
QY 201 LSKADYEKHKYACEVTHQGLSSPYTKSFNRGE 233
DB 181 LSKADYEKHKYACEVTHQGLSSPYTKSFNRGE 213

RESULT 10
US-09-453-234-90

Sequence 90, Application US/09453234
Publication No. US20030091995A1

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453, 234
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157, 415
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 90
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match 86.4%; Score 1057; DB 11; Length 224;
Best Local Similarity 95.8%; Pred. No. 7.5e-62;
Matches 204; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 21 EIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKPGQAPRLLYDTSNRTGIPA 80
DB 1 EIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKPGQAPRLLYDTSNRTGIPA 60
QY 81 RFSGSGGTDTLTLSISLEPEDFAVYCCQQRPNMPTFGQGTKEFKRTVAAPSVFIIPP 140
DB 61 RFSGSGGTDTLTLSISLEPEDFAVYCCQQRPNMPTFGQGTKEFKRTVAAPSVFIIPP 120
QY 141 SDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYLSSTLT 200
DB 121 SDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYLSSTLT 180
QY 201 LSKADYEKHKYACEVTHQGLSSPYTKSFNRGE 233
DB 181 LSKADYEKHKYACEVTHQGLSSPYTKSFNRGE 213

RESULT 11

US-09-453-234-36
Sequence 36, Application US/09453234
Publication No. US20030091995A1

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453, 234
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157, 415
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
US-09-453-234-36

Query Match 86.2%; Score 1054; DB 11; Length 224;
Best Local Similarity 95.8%; Pred. No. 1.2e-61;
Matches 204; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY	21	IIVLTOSPATISLSGCEAATLACRASCOTASRLAYOOPGAPRLIITYDTSNRAGIPA	80
Dp	1	EIVLTOSPATISLSGEPARITLSCRASQCVSYTLAQPGAPRLIITYDASNRAIGIPA	60
OY	81	RFGSGSGCTDEFTLSSISLEPEDFAVYYCOQRNMNMTFCQGTRVEKRTVAAPSVPFIIPP	140
Dp	61	RFGSGSGCTDEFTLSSISLEPEDFAVYYCQGRNMNMTFCQGRKEIKRTVAAPSVPFIIPP	120
OY	141	SDEOLKSTASYVCLLNFFYPREAVYOMKVDAALOSGNSQESYTDEDSDOSTYSLSSTLT	200
Dp	121	SDEOLKSTASYVCLLNFFYPREAVYOMKVDAALOSGNSQESTEDSDOSTYSLSSTLT	180
OY	201	LSKADYEKKHYACEVTTHOGLSSPPTKSPNRGE	233
Dp	181	LSKADYEKKHYACEVTTHOGLSSPPTKSPNRGE	213

```

RESULT 12
US-09-453-234-84
; Sequence 84, Application US/09453234
; Publication No. US20030091955A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRY
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84

```

```

Query Match      85.4%: Score 1045; DB 11: Length 224;
Best Local Similarity 94.8%: Pred. No. 4.5e-61;
Matches 202; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY      21 EIVLTGSPATLSLSPGERATLACRASQTASRYLAWYQOQKPGCAPRLLIYDTSNRATGIPA 80
Db      1 EIVLTGSPATLSLSPGERATLSCRASQSVSSYILAWYQOQKPGCAPRLLIYDASNRAGIIPA 60

QY      81 RFGSGSGCTDFTLSISLLEPEDFAVYYVYQOQRNMPWTFGCGTKVEFKRTVAAPSVFIIPP 140
Db      61 RFGSGSGCTDFTLLISLLEPEDFAVYYVYQOQRNMPWTFGCGTKVEIKRTVAAPSVFIIPP 120

QY      141 SDEQLKSGTASVACLLNNFYPREAKVQMKVQNALQSGSOSQSYMEQDSKDSYLSSTFLT 200
Db      121 SDEQLKSGTASVACLLNNFYPREAKVQMKVQNALQSGNSQESVTEQDSKDSYLSSTFLT 180

QY      201 LSKADYEKKHYACEVTHQGLSSPYTKSFNNGE 233
Db      181 LSKADYEKKHYACEVTHQGLSSPYTKSFNNGE 213

RESULT 13
US-09-453-234-46
: Sequence 46, Application US/09453234
: Publication No. US20030091955a1
: GENERAL INFORMATION:
: APPLICANT: Buechler, Joe
: APPLICANT: Valikits, Gunars
: APPLICANT: Gray, Jeff

```

```

: APPLICANT: Lonberg, Nils
: APPLICANT: Biosite Diagnostics, Inc.
: APPLICANT: Genpharm International
: TITLE OF INVENTION: Human Antibodies
: FILE REFERENCE: 020015-000110US
: CURRENT APPLICATION NUMBER: US/09/453,234
: CURRENT FILING DATE: 1999-12-01
: PRIOR APPLICATION NUMBER: US 60/157,415
: PRIOR FILING DATE: 1999-10-02
: NUMBER OF SEQ ID NOS: 112
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 46
: LENGTH: 224
: TYPE: PRT
: ORGANISM: Homo sapiens
: OTHER INFORMATION: MI-10L
US-09-453-234-46

```

	Query Match	85.3%	Score 1043:	DB 11:	Length 224:
	Best Local Similarity	93.9%:	Pred. No. 6.1e-61:		
	Matches	Conservative	6:	Mismatches	7:
				Indels	0:
				Gaps	0:
Oy	21	EIVLTQSPATLSLSPGERATLACRAQTASRYLAWYQQK _{PL} QAPRLITYDSNRATGIPA	80		
	:::::				
Dd	1	DVMTQSPATLSISPGERATLSCRASGVSSYLAWYQQK _{PI} QAPELLIYDASNRRATGIPA	60		
Oy	81	RFSSSGSDTDTLLSISSLEPEDFANYYYCOQRFNPMWTGCQITKVEFKRTVAAPSFTIRPP	140		
Dd	61	RFSGGSTDTTLTISSLEPEDFAYYYCOQRSMNPPTTGITKEIKRTVAAPSFTIRPP	120		
Oy	141	SDEOLKSSTASAVCLLNMFYPREAKVQKVNALQSGNSQLSVTEQDSKSDSYLSLSLT	200		
Dd	121	SDEQLKSGTASAVCLLNMFYPREAKVQKVNALQSGNSQLSVTEQDSKSDSYLSLSLT	180		
Oy	201	LSKADYEKNKYACEVTHQGLSSPYTKSFNGE	233		
Dd	181	LSKADYEKNKYACEVTHQGLSSPYTKSFNGE	213		

RESULT 14
US-10-216-484-107
Sequence 107, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976A1ufusa
APPLICANT: Haruyama, Hideoyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takamaki, Ikuko
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126C1P/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 107
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antl-body
US-10-216-484-107

Query Match	84.0%	Score 1027:	DB 15;	Length 238;
Best Local Similarity	84.5%;	Pred. No. 7.1e-60;		
Matches 201; Conservative	11;	Mismatches 22;	Indels 4;	Gaps 1;
Oy	1	MEADQLELLMLDPDTGETIVLTQSAPATISLSEGEARTACRARSQT---	ASRYLAWY	56
	:: ::	::: ::	:::	:::

```

Dh 1 MERTDILLAWLILLMVGSGTIVLNGSPETLSLBSGBRATLSCKAKSGSVDDIGDSYNNWY 60
Qy 57 QQRGQAPRLLIYDTSNRATGPAPRSGSGSTDTFTLSSLEPEDFAVYVCOGRFMPW 116
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dh 61 QQRGQAPRLLIYAAASNTLESIGIPDRFSGSGSTDTFTLISLEPEDFAVYVCOOSNEPR 120
Qy 117 TFGQGTVEEKKRRVAAVSFIFFPSPDEOLKSTASVCLLNFFYREAKKQVMKVDNALOS 176
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dh 121 TFGQGTLEKKRRVAAVSFIFFPSPDEOLKSTASVCLLNFFYREAKKQVMKVDNALOS 180
Qy 177 GNSQESVTEEDSKDSYFSLSTLTLSKADYEKKHYACEVTHOGSLSPVTKSPFNRGEC 234
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dh 181 GNSQESVTEEDSKDSYFSLSTLTLSKADYEKKHYACEVTHOGSLSPVTKSPFNRGEC 238

```

RESULT 15

```

US-09-859-053-30
: Sequence 30, Application US/098595053
: Patent No. US20020102658A1
: GENERAL INFORMATION:
: APPLICANT: Tsuji, Takashi
: APPLICANT: Tezuka, Katsunari
: APPLICANT: Hori, No. US20020102658A1uaki
: TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
: TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE
: TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
: FILE REFERENCE: 06501-079001
: CURRENT APPLICATION NUMBER: US/09/859, 053
: CURRENT FILING DATE: 2001-05-16
: PRIOR APPLICATION NUMBER: JP 2001-99508
: PRIOR FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: JP 2000-147116
: PRIOR FILING DATE: 2000-05-18
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 236
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-859-053-30

```

Query Match	83.08;	Score 1015;	DB 10;	Length 236;
Best Local Similarity	82.58;	Pred. No. 4.3e-59;		
Matches 193; Conservative	18;	Mismatches 23;	Indels 0;	Gaps 0;

[illegible]

Search completed: September 12, 2003, 13:06:07
Job time : 16.2034 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:58:39 ; Search time 13.2203 Seconds
(without alignments)
748.902 Million cell updates/sec

Title: US-09-848-832-4

Perfect score: 1223

Sequence: 1 MEAPRQLLEFLLLMLPDTTG.....EYTHGGLSPYTKSRNGEC 234

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCRTS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1056	86.3	234	3	US-09-049-672A-6
2	993	81.2	234	4	US-09-740-002-24
3	982	80.3	240	4	US-09-301-593-36
4	978.5	80.0	235	1	US-08-276-852-153
5	978.5	80.0	235	1	US-08-899-575-153
6	978.5	80.0	235	1	US-08-899-575-153
7	978.5	80.0	235	5	PCRT-US95-08743-153
8	978	80.0	235	5	US-08-812-586-16
9	978	80.0	235	4	US-09-535-832A-17
10	970.5	79.4	241	2	US-07-916-098A-56
11	962.5	78.7	214	2	US-08-480-753-6
12	962.5	78.7	214	3	US-09-041-889-11
13	962.5	78.7	214	3	US-08-837-058-11
14	962.5	78.7	214	4	US-09-417-264-11
15	962.5	78.7	214	4	US-09-315-926A-79
16	955.5	78.1	239	3	US-08-487-550-6
17	955.5	78.1	239	4	US-09-526-098-6
18	955	78.1	236	4	US-08-157-101A-5
19	954.5	78.0	233	4	US-09-485-737B-69
20	946.5	77.4	235	3	US-09-171-945-97
21	946	77.4	214	1	US-08-458-516-12
22	945.5	77.3	234	4	US-09-740-002-26
23	944	77.2	232	1	US-08-704-744-80
24	942	77.0	218	5	PCRT-US96-13152-2
25	942	77.0	240	4	US-09-301-593-28
26	941.5	77.0	233	2	US-07-934-373C-25
27	941.5	77.0	233	3	US-08-437-642B-25

28	941.5	77.0	233	4	US-08-146-206C-25	Sequence 25, Appl
29	941.5	77.0	233	5	PCRT-US93-07832-25	Sequence 25, Appl
30	941	76.9	215	2	US-08-480-753-8	Sequence 8, Appl1
31	938	76.7	214	2	US-07-934-373C-39	Sequence 39, Appl1
32	938	76.7	214	3	US-08-437-642B-39	Sequence 39, Appl1
33	938	76.7	214	5	PCRT-US93-07832-39	Sequence 39, Appl1
34	937	76.6	214	2	US-07-934-373C-40	Sequence 40, Appl
35	937	76.6	214	2	US-08-788-800-11	Sequence 40, Appl
36	937	76.6	214	3	US-08-437-642B-40	Sequence 11, Appl
37	937	76.6	214	3	US-09-097-309-2	Sequence 2, Appl1
38	937	76.6	214	3	US-09-097-171A-2	Sequence 2, Appl1
39	937	76.6	214	3	US-09-460-587-2	Sequence 2, Appl1
40	937	76.6	214	5	PCRT-US93-07832-40	Sequence 40, Appl
41	937	76.6	237	3	US-09-097-309-6	Sequence 6, Appl1
42	937	76.6	237	3	US-09-097-171A-10	Sequence 10, Appl
43	937	76.6	237	3	US-09-422-712B-2	Sequence 2, Appl1
44	937	76.6	237	3	US-09-607-756-2	Sequence 2, Appl1
45	937	76.6	237	4	US-09-460-587-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-049-672A-6
Sequence 6, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guebler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLSUCT01

CLONE: 2280869
US-09-049-672A-6

Query Match 86.3%; Score 1056; DB 3; Length 234;
Best Local Similarity 85.9%; Pred. No. 7.6e-79;
Matches 201; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
DB 1 MEAPQALLFLLLMLPDSFGEIVMTQSPALVSLSPGERATLSCRASQTSIGSTIAYYQGRP 60
QY 61 GOAPRLLYDTSNRATGTPARFSGSGSTDTLTSLSSLEPEDFAYVYCOQRFNMPWTGQ 120
DB 61 GQSPRLLYGASTRATGVPPRFSGSGSGTEFTLFISSLSQSDFDALYYCOQYKGMPLTFGG 120
QY 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQMKVDNALQSGNSQ 180
DB 121 GTRQIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQMKVDNALQSGNSQ 180
QY 181 ESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
DB 181 ESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 2
US-09-740-002-24
Sequence 24, Application US/09740002
Patent No. 6537809

GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
US-09-740-002-24

Query Match 81.2%; Score 993; DB 4; Length 234;
Best Local Similarity 80.8%; Pred. No. 1e-73;
Matches 189; Conservative 16; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
DB 1 MEAPQALLFLLLMLRGRACDIOMTQSPSSLSASVGRVITTCRAGRASIAYSLWYQHKP 60
QY 61 GOAPRLLYDTSNRATGTPARFSGSGSTDTLTSLSSLEPEDFAYVYCOQRFNMPWTGQ 120
DB 61 GKAPRLLYAGSNHNRGVPSRFSGSGSTDTLTSLSSLEPEDFAYVYCOQRFNMPWTGQ 120
QY 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQMKVDNALQSGNSQ 180
DB 121 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQMKVDNALQSGNSQ 180
QY 181 ESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
DB 181 ESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 3
US-09-301-593-36
Sequence 36, Application US/09301593A

Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Retlig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Productibility
FILE REFERENCE: 0652,1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-36

Query Match 80.3%; Score 982; DB 4; Length 240;
Best Local Similarity 78.8%; Pred. No. 8.4e-73;
Matches 189; Conservative 22; Mismatches 23; Indels 6; Gaps 1;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQ-----ASRLA 54
DB 1 METDLLMVLVLLWPSSGSDIVMTQSPDSLAVSLGGERATINCKSSQSLYSRNQKNTLA 60
QY 55 WYQOKPGQAPRLLYDTSNRATGTPARFSGSGSDTFLTSLSSLEPEDFAYVYCOQRFNMP 114
DB 61 WYQOKPGQAPRLLYDTSNRATGTPARFSGSGSDTFLTSLSSLEPEDFAYVYCOQRFNMP 120
QY 115 PWTGQGTVEFKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQMKVDNAL 174
DB 121 PLTFGQGTVEIKRTVAAPSVFIFPPSDEQLKSGTASVYCLINNFYPREAKVQMKVDNAL 180
QY 175 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
DB 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 4
US-08-276-852-153
Sequence 153, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994


```

? APPLICATION NUMBER: US 08/276,852
? FILING DATE: 18-JUL-1994
? APPLICATION NUMBER: US 08/178,302
? FILING DATE: 30-SEP-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/954,148
? FILING DATE: 30-SEP-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Fitting, Thomas
? REGISTRATION NUMBER: 34,163
? REFERENCE/DOCKET NUMBER: SCRI452P
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619-554-2937
? TELEFAX: 619-554-6312
? INFORMATION FOR SEQ ID NO: 153:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 235 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-899-575-153

```

	80.0%:	Score	978.5:	DB 1:	Length	235:			
Query Match									
Best Local Similarity	82.1%:	Pred. No.	1.6e-72:						
Matches	193:	Conservative	14:	Mismatches	27:	Indels	1:	Gaps	1:
OY	1	MEADQALLFLLLMLPDTGEIVLTQSPATLSLPEGERATLACRASQT-AKRYTAWDYOK	59						
Db	1	MGVPTQVLGLLLMTDARCEIVLTQSGLTSLSPGEGATFSSRSHSISRRAWYOHK	60						
OY	60	PGCAPELLIDTSNRATGIPARFGSGSGCTFTLSTLSLEPEDFDALYYICQVYGASSSYFG	119						
Db	61	PGCAPRLVIYGVNSRRASGISDRFGSGSGDTFTLTITRVESDPALYYICQVYGASSSYFG	120						
OY	120	QGTRVEEKRTVAADVSEIFPPSDQLKSQTASVYCLNNFFYPREAKYQMKVDNALQSGNS	179						
Db	121	QGTLEKKRTVPAPSVSEFPSPDQLKSGTASVYCLNNFFYPREAKYQMKVDNALQSGNS	180						
OY	180	QESTVTEDDSKDSYTLSTLTKSAVDKEKHVVACEYTHQGLSSPYTKSFNRGEC	234						
Db	181	QESTVTEDDSKDSYTLSTLTKSAVDKEKHVVACEYTHQGLSSPYTKSFNRGEC	235						

```

: RESULT 7
: PCT-US95-08743-153
: Sequence 153 Application PC/TUS9508743
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
: TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
: NUMBER OF SEQUENCES: 170
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patentin Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/08743
: FILING DATE: 11-JUL-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/276,852
: FILING DATE: 18-JUL-1994
: INFORMATION FOR SEQ ID NO: 153:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 235 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: CTT-US95-08743-153

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Query Match	80.0%	Score	978.5	DB	5	Length	235
Similarity	82.1%	Pred. No.	1.6e-72				
Best Local							
Matches	193	Conservative	14	Mismatches	27	Indels	1
						Gaps	1

[illegible]

RESULT 8
US-08-812-586-16
; Sequence 16, Application US/08812586

GENERAL INFORMATION:
APPLICANT: Martin David Tilson
TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSA (AAA)
TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/53862-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-812-586-16

[illegible]

```

Db      123 GTRKEIKRTVAAPSVFIFPPSDEQKLSKSTASVYGLLNFFYPREAKVQWKVDNALQSGNSQ 182
        181 ESVTQDSKSTSTYSLSSTITLTKADYEKKYVACEYTHGSLSPYTKSFNRGE 233
        183 ESVTQDSKSTSTYSLSSTITLTKADYEKKYVAGEVTHGSLSPYTKSFNRGE 235

```

RESULT 9

```

US-09-535-832A-17
; Sequence 17, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; FILE REFERENCE: 53862-A2
; CURRENT APPLICATION NUMBER: US/09/535,832A
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-17

```

```

Query Match      80.0%; Score 978; DB 4; Length 235;
Best Local Similarity 84.1%; Pred. No. 1.7e-72;
Matches 196; Conservative 8; Mismatches 29; Indels 0; Gaps 0;

```

```

QY      1 MEAPQDLFLLLMLPDTGGEIVLTQSPATLSLPEPERATLACRAQTASRIYATQKRP 60
        3 MEVPAQLLGLLLMLPGARCAIRIAQSPSLASTDRTVITCRASQISNTLAWYQKRP 62
QY      61 GOAPRLIYDTSNRATGIPARFSGSGGTFTLSSLEPEDFAVYCCOREFNMWPTFGQ 120
        63 GQAPRLIYDASSRAIGIRDRSGSGGTFTLISRLPEDEPAVYGGQYGSPLTFGG 122
Db      121 GTRVEKRTVAAPSVFIFPPSDEQKLSGTASVYGLLNFFYPREAKVQWKVDNALQSGNSQ 180
        123 GTRVEIKRTVAAPSVFIFPPSDEQKLSGTASVYGLLNFFYPREAKVQWKVDNALQSGNSQ 182
QY      181 ESVTQDSKSTSTYSLSSTITLTKADYEKKYVACEYTHGSLSPYTKSFNRGE 233
        183 ESVTQDSKSTSTYSLSSTITLTKADYEKKYVAGEVTHGSLSPYTKSFNRGE 235
Db

```

RESULT 10

```

US-07-916-098A-56
; Sequence 56, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, AHC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-916-098A-56

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Query Match      79.4%; Score 970.5; DB 2; Length 241;
Best Local Similarity 79.2%; Pred. No. 7.3e-72;
Matches 190; Conservative 18; Mismatches 25; Indels 7; Gaps 2;

```

```

QY      1 MEAPQDLFLLLMLPDTGGEIVLTQSPATLSLPEPERATLACRA-----SQTASRIYA 54
        3 MEVPAQLLGLLLMLPGARCAIRIAQSPSLASTDRTVITCRASQISNTLAWYQKRP 62
QY      55 WYQKRGQAPRLIYDTSNRATGIPARFSGSGGTFTLSSLEPEDFAVYCCOREFNMWPTFGQ 114
        63 WYQKRGQAPRLIYDTSNRATGIPARFSGSGGTFTLSSLEPEDFAVYCCOREFNMWPTFGQ 122
Db      115 PMTGGGTVEKRTVAAPSVFIFPPSDEQKLSGTASVYGLLNFFYPREAKVQWKVDNAL 174
        123 R-TFGGTVEKRTVAAPSVFIFPPSDEQKLSGTASVYGLLNFFYPREAKVQWKVDNAL 181
QY      175 QSGNSESVTQDSKSTSTYSLSSTITLTKADYEKKYVACEVTHGSLSPYTKSFNRGEC 234
        182 QSGNSESVTQDSKSTSTYSLSSTITLTKADYEKKYVACEVTHGSLSPYTKSFNRGEC 241
Db

```

RESULT 11

```

US-08-480-753-6
; Sequence 6, Application US/08480753
; Patent No. 5830675
; GENERAL INFORMATION:
; APPLICANT: Targan M.D., Stephan R.
; APPLICANT: Viorich Ph.D., Alda M.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
; TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF
; TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS, OR
; TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wendy A. Whiteford, Esq.
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25

```

REGISTRATION NUMBER: 31,815

TYPE: amino acid

TOPLOGY: linear


```
MOLECULE TYPE: protein
US-08-837-058-11

Query Match      78.7%; Score 962.5; DB 3; Length 214;
Best Local Similarity 88.7%; Pred. No. 2.8e-71;
Matches 188; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 24 LTQSPATLSLSPGERATLACRASQTS-RYLAWYQOKPGQAPRLIYDTSNRATGIPARF 82
DB 3 LTQSPGTLSTLSPGERATLSCRASQRISTSLAWYQOKPGQAPRLIYDTSNRATGIPARF 62
QY 83 SGGSGTDFTLTSLISLEPEDFAVYCCQGRFNMWTFGGGTVEKRYVAAPSVFTFPSPD 142
DB 63 SASWSGTDFTLTSLISLEPEDFAVYCCQHYGSGSPMTFGGQTKVEIKRTVAAPSVFTFPSPD 122
QY 143 EQLKSGTASVYCLLNFPYPRKAYQWKVDNALQSGNSQSEYVEODSKDSTYSLSTLTLS 202
DB 123 EQLKSGTASVYCLLNFPYPRKAYQWKVDNALQSGNSQSEYVEODSKDSTYSLSTLTLS 182
QY 203 KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
DB 183 KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 14
US-09-417-264-11
; Sequence 11, Application US/09417264
; Patent No. 6537768
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Chavay, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,889
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-417-264-11

Query Match      78.7%; Score 962.5; DB 4; Length 214;
Best Local Similarity 88.7%; Pred. No. 2.8e-71;
Matches 188; Conservative 5; Mismatches 18; Indels 1; Gaps 1;
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QY 24 LTQSPATLSLSPGERATLACRASQTS-RYLAWYQOKPGQAPRLIYDTSNRATGIPARF 82
DB 3 LTQSPGTLSTLSPGERATLSCRASQRISTSLAWYQOKPGQAPRLIYDTSNRATGIPARF 62
QY 83 SGGSGTDFTLTSLISLEPEDFAVYCCQGRFNMWTFGGGTVEKRYVAAPSVFTFPSPD 142
DB 63 SASWSGTDFTLTSLISLEPEDFAVYCCQHYGSGSPMTFGGQTKVEIKRTVAAPSVFTFPSPD 122
QY 143 EQLKSGTASVYCLLNFPYPRKAYQWKVDNALQSGNSQSEYVEODSKDSTYSLSTLTLS 202
DB 123 EQLKSGTASVYCLLNFPYPRKAYQWKVDNALQSGNSQSEYVEODSKDSTYSLSTLTLS 182
QY 203 KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
DB 183 KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 15
US-09-315-926A-79
; Sequence 79, Application US/09115926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent version 3.0
; SEQ ID NO 79
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(236)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79

Query Match      78.7%; Score 962.5; DB 4; Length 236;
Best Local Similarity 82.9%; Pred. No. 3.2e-71;
Matches 194; Conservative 11; Mismatches 24; Indels 5; Gaps 3;

QY 6 QLLFLLMLP---DTGELIVLTQSPATLSLSPGERATLACRASQTS-ASRYLAWYQOKPG 61
DB 3 KLLFALPLVLPYFYSHALETTLTQSPGTLSTLSPGAGATLSCRASQSVSSRNLAHWYQOKPG 62
QY 62 QAPRLIYDTSNRATGIPARFSGSGSGGTFTLTSLISLEPEDFAVYCCQGRFNMWTFGGQ 121
DB 63 QAPRLIYDTSNRATGIPARFSGSGSGGTFTLTSLISLEPEDFAVYCCQGRFNMWTFGGQ 122
QY 122 TKVEKRR-TVAAPSVFTFPSPDEQLKSGTASVYCLLNFPYPRKAYQWKVDNALQSGNSQ 180
DB 123 TKVEIKRGTVAAPSVFTFPSPDEQLKSGTASVYCLLNFPYPRKAYQWKVDNALQSGNSQ 182
QY 181 ESVTQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
DB 183 ESVTQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

Search completed: September 12, 2003, 13:05:15
Job time : 15.2203 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2003, 12:56:44 : Search time 40.6525 Seconds
(without alignments)
1485.376 Million cell updates/sec

Title: US-09-848-832-4

Perfect score: 1223

Sequence: 1 MEAPAOLEFLLLMLPDTG.....EYTHQGLSSPYTKSFNRGRC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvivirus:*
16: sp.bacteriophage:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1090	89.1	234	4	Q8NEK1
2	961.5	78.6	239	4	Q8NEK0
3	956.5	78.2	239	4	Q8TCD0
4	729	59.6	238	11	Q99M37
5	724	59.2	234	11	Q8VCP0
6	720	58.9	238	11	Q8VCI6
7	709	58.0	234	11	Q8R062
8	702.5	57.4	239	11	Q8K0F8
9	701	57.3	234	11	Q91WF8
10	700.5	57.3	239	11	Q8VCS5
11	690	56.4	233	11	Q91WS9
12	676.5	55.3	235	11	Q91W12
13	676	55.3	234	11	Q91A15
14	655	53.6	234	11	Q8R028
15	458.5	37.5	233	4	Q8TBC9
16	454.5	37.2	234	4	Q8N355

17	453	37.0	108	4	Q9UL83	Q9UL83 homo sapien
18	447	36.5	236	4	Q8NEJ1	Q8NEJ1 homo sapien
19	443	36.2	237	4	Q8W7U6	Q8W7U6 homo sapien
20	440.5	36.0	109	4	Q9UL78	Q9UL78 homo sapien
21	440	35.9	237	4	Q8W0K4	Q8W0K4 homo sapien
22	438.5	35.9	233	4	Q8N5F4	Q8N5F4 homo sapien
23	431.5	35.3	109	4	Q9UL85	Q9UL85 homo sapien
24	430.5	35.2	109	4	Q9UL86	Q9UL86 homo sapien
25	410.5	33.6	236	4	Q96E61	Q96E61 homo sapien
26	404	33.0	108	4	Q9UL77	Q9UL77 homo sapien
27	402	32.9	116	4	Q96PF6	Q96PF6 homo sapien
28	393.5	32.2	134	11	Q8VDD0	Q8VDD0 mus musculu
29	392	32.1	108	4	Q9UL79	Q9UL79 homo sapien
30	390	31.9	233	4	Q96TF9	Q96TF9 homo sapien
31	380.5	31.1	107	4	Q96SA9	Q96SA9 homo sapien
32	379.5	31.0	112	11	Q8K1F2	Q8K1F2 mus musculu
33	379.5	31.0	114	11	Q8K1F1	Q8K1F1 mus musculu
34	379	31.0	240	4	Q8W0K3	Q8W0K3 homo sapien
35	378	30.9	235	11	Q99M11	Q99M11 mus musculu
36	377.5	30.9	112	11	Q8K1F3	Q8K1F3 mus musculu
37	368	30.1	108	4	Q9UL70	Q9UL70 homo sapien
38	362.5	29.6	107	4	Q9UL81	Q9UL81 homo sapien
39	358.5	29.3	106	5	Q9UL10	Q9UL10 schistosoma
40	357	29.2	109	11	Q920E6	Q920E6 mus musculu
41	357	29.2	111	11	Q920E9	Q920E9 mus musculu
42	357	29.2	298	11	Q9QYF0	Q9QYF0 mus musculu
43	352	28.8	114	4	Q9UL80	Q9UL80 homo sapien
44	343.5	28.1	112	11	Q8K1F0	Q8K1F0 mus musculu
45	338	27.6	127	11	Q925S9	Q925S9 mus musculu

ALIGNMENTS

RESULT 1					ALIGNMENTS				
ID	Q8NEK1	PRELIMINARY:	PRT:	234 AA.					
AC	Q8NEK1								
DT	01-OCT-2002 (TREMBLrel. 22, Created)								
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)								
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)								
DE	Hypothetical protein.								
OS	Homo sapiens (human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Lung;								
RA	Strausberg R.;								
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; BC030813; AA030813.1; -								
DR	InterPro: IPR007110; Ig-1-like.								
DR	InterPro: IPR003597; Ig_c1.								
DR	InterPro: IPR003006; Ig_MHC.								
DR	InterPro: IPR003596; Ig_V.								
DR	Pfam: PF00047; Ig_2.								
DR	SMART: SM00407; Igc1; 1.								
DR	SMART: SM00406; Igv; 1.								
DR	PROSITE: PS00835; IG_LIKE; 2.								
DR	PROSITE: PS00290; IG_MHC; 1.								
KW	Hypothetical protein.								
SQ	SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;								
Query Match 89.1%; Score 1090; DB 4; Length 234;									
Best local Similarity 88.5%; Pred. No. 4.6e-96;									
Matches 207; Conservative 15; Mismatches 12; Indels 0; Gaps 0;									
QY	1	MEAPAOLEFLLLMLPDTGTEIVLTQSPATLSLSPERATLACRASQTSRYLAWYQARP 60							
DB	1	MEAPAOLEFLLLMLPDTGTEIVLTQSPATLSVSPERATLSCRASQTSRYLAWYQARP 60							
QY	61	GQAPRLIYDTSNRATGIRARFSGSGSDFTLISLSLEFEDRAVYCCQRRFWMPPTFQ 120							

```

Db      61 GOSPELVITYGASSRASGVAPARSGSGSTEFFLTITSSIQSEFPAYVYCOQYKMKPHTEGQ 120
Oy      121 GTKVEFRRTVAAPSVFIFPPSDEOLKSGTASVYVCLNNFYPREAVQVKVNDALQSGMSQ 180
Db      121 GTKLDIKRTVAAPSVFIFPPSDEOLKSGTASVYVCLNNFYPREAVQVKVNDALQSGMSQ 180
Oy      181 ESYTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
Db      181 ESYTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

```

RESULT 2

```

O8NEKO PRELIMINARY: PRT: 239 AA.
AC O8NEKO:
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC030814; AAH30814.1; -
DR InterPro: IPR007110; Iq-like.
DR InterPro: IPR003597; Iq-cl.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq-V.
DR Pfam: PF00047; Iq; 2.
DR SMART: SM00407; Iqcl; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; Iq_LIKE; 2.
DR PROSITE: PS00290; Iq_MHC; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

```

Query Match 78.6%; Score 961.5; DB 4; Length 239;
 Best Local Similarity 77.4%; Pred. No. 9,1e-84;
 Matches 185; Conservative 20; Mismatches 29; Indels 5; Gaps 1;

```

Oy      1 MEAPQQLFLLLMLPDTTGETIVLTQSPATLSLPGERATLACRASQT-----ASRYLAW 55
Db      1 MRLPAQLGLMLMWSSGSDVMTQSPVLTGEPASISCRSSQLHSDGYNILDM 60
Oy      56 YQKPGQAPRLIIYDTSNRATGIPARFSGSGSGTDFTLISLSLEPEDFAVYVCOQRFNMP 115
Db      61 YLQKGGSPOLLIVTGSNRRASGVPRFSGSGSGTDFTLKISKVEADVGIIYCMQGLQTP 120
Oy      116 WFGGQGVYERKRYVAAPSVFIFPPSDEQLKSGTASVYVCLNNFYPREAVQVKVNDALQ 175
Db      121 QTFGGGTVEIKRYVAAPSVFIFPPSDEQLKSGTASVYVCLNNFYPREAVQVKVNDALQ 180
Oy      176 SGNSESVTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
Db      181 SGNSESVTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

```

RESULT 3

```

O8TCDO PRELIMINARY: PRT: 239 AA.
AC O8TCDO:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC022362; AAH22362.1; -
DR InterPro: IPR007110; Iq-like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq-V.
DR Pfam: PF00047; Iq; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; Iq_LIKE; 2.
DR PROSITE: PS00290; Iq_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; F4CEDC3A3B03871D CRC64;

```

Query Match 78.2%; Score 956.5; DB 4; Length 239;
 Best Local Similarity 75.3%; Pred. No. 2.7e-83;
 Matches 180; Conservative 28; Mismatches 26; Indels 5; Gaps 1;

```

Oy      1 MEAPQQLFLLLMLPDTTGETIVLTQSPATLSLPGERATLACRASQT-----ASRYLAW 55
Db      1 MRLPAQLGLMLMWSSGSDVMTQSPVLTGEPASISCRSSQLHSDGYNILDM 60
Oy      56 YQKPGQAPRLIIYDTSNRATGIPARFSGSGSGTDFTLISLSLEPEDFAVYVCOQRFNMP 115
Db      61 FQKRGQSPRLIIYVSNRDSGVPRFSGSGSGTDFTLKIRVEADVGIVFCMQGTNMP 120
Oy      116 WFGGQGVYERKRYVAAPSVFIFPPSDEQLKSGTASVYVCLNNFYPREAVQVKVNDALQ 175
Db      121 STFGGQTKLEIKRYVAAPSVFIFPPSDEQLKSGTASVYVCLNNFYPREAVQVKVNDALQ 180
Oy      176 SGNSESVTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
Db      181 SGNSESVTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

```

RESULT 4

```

O99M37 PRELIMINARY: PRT: 238 AA.
AC O99M37:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC002035; AAH02035.1; -
DR HSP: P01679; 2FBJ.
DR InterPro: IPR007110; Iq-like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq-V.
DR Pfam: PF00047; Iq; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; Iq_LIKE; 2.
DR PROSITE: PS00290; Iq_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

```

Query Match 59.6%; Score 729; DB 11; Length 238;
 Best Local Similarity 56.5%; Pred. No. 1.5e-61;
 Matches 135; Conservative 44; Mismatches 54; Indels 6; Gaps 2;

```

Oy      1 MEAPQQLFLLLMLPDTTGETIVLTQSPATLSLPGERATLACRASQT-----ASRYLAW 55
Db      1 MRLPAQLGLMLMWSSGSDVMTQSPVLTGEPASISCRSSQLHSDGYNILDM 60

```


Best Local Similarity 57.5%; Pred. No. 1.5e-56;
Matches 123; Conservative 37; Mismatches 54; Indels 0; Gaps 0;

```
OY 21 EIVLTOSPATLSLSPGERATLACRASOTASRYLAWYQOQPGQAPRLLYDTSNRATGPA 80
Db 1 DIQLQSSSWASLGERVYTCRASQDINSTLSWFOOKPKSPPTLLYRANRLVDGVP 60
OY 81 RFSGSGCTDPTLSTLSLEPEDFAVYCCQRFNFWPTFGCTKVEFKRTVAAPSVFI 140
Db 61 RFSGSGGQDYSLRTSLSEYEDMGITYCLOQDEPFRTGSGTKLEIKRADAAPTSTFP 120
OY 141 SDEQKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYSLSSTLT 200
Db 121 SSEQLTSGGASVCFLLNFFPKDINVKWKIDGSEKQNGVLNMTQDSKSTYSMSSTLT 180
OY 201 LSKADYEKKYACEVTHQGLSSPTKSFNREGC 234
Db 181 LTKDEYERHNSITCEATHTKSTSTPLVKCFNRNEC 214
```

RESULT 14

O8R028 PRELIMINARY: PRT: 234 AA.

```
ID O8R028.
AC O8R028.
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028540; AAH28540.1;
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0AEE CRC64;
```

Query Match 53.6%; Score 655; DB 11; Length 234;

Best Local Similarity 54.8%; Pred. No. 1.8e-54;
Matches 126; Conservative 33; Mismatches 71; Indels 0; Gaps 0;

```
OY 5 AQLFLLLMLPDTGELVLTQSPATLSLSPGERATLACRASOTASRYLAWYQOQPGQAP 64
Db 5 APLSLLLLCVDSORAEFTVYQSPASLSVATGEKVTIRCTSIDDDMMNMYQOKPGEP 64
OY 65 RLIIYDTSNRATGIPARFSGSGCTDPTLSTLSLEPEDFAVYCCQRFNFWPTFGG 124
Db 65 KLLISEGNTLRPGVPSRFSSSGSGYGTDFEVTIENTLSEVDADYCYCLOSDNMP 124
OY 125 EFKRTVAAPSVFIPEPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQSV 184
Db 125 ELKADAPTYSTIPPSSEELQANKATLVCLISDFPGAVTVAMKADSSPVKAG-- 184
OY 185 EQDSKSTYSLSSTLTLSKADYEKKYACEVTHQGLSSPTKSFNREGC 234
Db 185 DQDSKSTYSMSSTLTLLTKDEYERHNSITCEATHTKSTSTPLVKSFNRNEC 234
```

RESULT 15

O8TBC9 PRELIMINARY: PRT: 233 AA.

```
ID O8TBC9.
AC O8TBC9.
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
```

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

```
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH22823.1;
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
```

Query Match 37.5%; Score 458.5; DB 4; Length 233;

Best Local Similarity 43.1%; Pred. No. 1.1e-35;
Matches 100; Conservative 41; Mismatches 82; Indels 9; Gaps 6;

```
OY 7 LLLFLLLMLPDTGELVLTQSPATLSLSPGERATLACRASOTASRYLAWYQOQPGQAPRL 66
Db 6 LLLPLRLCTGSEASVELTQ--PPSVSPGQTARITGSGDALPQYAYWYQKPGQAPVL 64
OY 67 LIYDTSNRATGIPARFSGSGCTDPTLSTLSLEPEDFAVYCCQ--QRFNFWPTFGG 124
Db 65 VIYKDNEPSPGIPERFSSSSGSGTYVTLLISGVQAEDEADYCCQADSSGTYWVG 124
OY 125 E-FKRTVAAPSVFIPEPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQSV 182
Db 125 TVLQGPRAAPSVYTLFPSSSEELQANKATLVCLISDFPGAVTVAMKADSSPVKAG-- 182
OY 183 VTQDSKSTYSLSSTLTLSKADYEKKYACEVTHQGLSSPTKSFNREGC 234
Db 183 TTPSKQSNKKYAAASSYSLTLPTEQWKSHKSYSCQVTHG--STVEKTVAPTEC 232
```

Search completed: September 12, 2003, 13:03:29
Job time : 42.6525 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:47:03 : Search time 9.91525 Seconds
(without alignments)
1109.830 Million cell updates/sec

Title: US-09-848-832-4
Perfect score: 1223
Sequence: 1 MEAPQQLLELLMLPDTTG.....EYTHQGLSSPYTKSFNRGRC 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	46.4	115	KVJ1_HUMAN	P04433 homo sapien
2	563.5	46.1	129	KVJ3H_HUMAN	P04207 homo sapien
3	562.5	46.0	129	KVJ3M_HUMAN	P18136 homo sapien
4	553.5	45.3	129	KVJ3L_HUMAN	P18135 homo sapien
5	548	44.8	106	KAC_HUMAN	P01834 homo sapien
6	529	43.3	128	KVJ3K_HUMAN	P06311 homo sapien
7	494.5	36.7	109	KVJ3J_HUMAN	P04434 homo sapien
8	448.5	36.7	109	KVJ3D_HUMAN	P01620 homo sapien
9	448.5	36.2	109	KVJ3E_HUMAN	P01622 homo sapien
10	442.5	36.2	109	KVJ3F_HUMAN	P01624 homo sapien
11	441.5	36.1	109	KVJ3G_HUMAN	P04206 homo sapien
12	441.5	36.1	109	KVJ3H_HUMAN	P06313 homo sapien
13	432	35.3	134	KVJ3C_HUMAN	P06319 homo sapien
14	427.5	35.0	108	KVJ3A_HUMAN	P01619 homo sapien
15	427.5	35.0	133	KVJ2E_HUMAN	P04432 homo sapien
16	418	34.2	129	KVJ1E_HUMAN	P04431 homo sapien
17	417	34.1	129	KVJ1W_HUMAN	P01661 mus musculu
18	414	33.9	131	KVJ1E_MOUSE	P01658 mus musculu
19	409	33.4	132	KVJ3E_MOUSE	P01602 homo sapien
20	406	33.2	117	KVJ1J_HUMAN	P01605 homo sapien
21	400	32.7	108	KVJ1M_HUMAN	P01621 homo sapien
22	399.5	32.7	100	KVJ3C_HUMAN	P01600 homo sapien
23	393	32.1	108	KVJ1H_HUMAN	P06313 homo sapien
24	391.5	32.0	133	KVJ4B_HUMAN	P01594 homo sapien
25	387	31.6	108	KVJ1B_HUMAN	P04430 homo sapien
26	386	31.6	108	KVJ1V_HUMAN	P01603 homo sapien
27	384	31.4	108	KVJ4A_HUMAN	P01625 homo sapien
28	381	31.2	114	KVJ4K_HUMAN	P01595 homo sapien
29	379	31.0	108	KVJ1C_HUMAN	P01608 homo sapien
30	378	30.9	108	KVJ1P_HUMAN	P01637 mus musculu
31	377	30.8	128	KVJ5E_MOUSE	P01633 mus musculu
32	377	30.8	149	KVJ5A_MOUSE	P01596 homo sapien
33	376.5	30.8	107	KVJ1D_HUMAN	

34	376	30.7	108	1	KVJ1N_HUMAN	P01606 homo sapien
35	376	30.7	136	1	KVJ5B_MOUSE	P01634 mus musculu
36	375	30.7	108	1	KVJ1E_HUMAN	P01597 homo sapien
37	374	30.6	108	1	KVJ1L_HUMAN	P01604 homo sapien
38	374	30.6	108	1	KVJ1R_HUMAN	P01610 homo sapien
39	372	30.4	111	1	KVJ3O_MOUSE	P01667 mus musculu
40	369	30.2	108	1	KVJ1O_HUMAN	P01607 homo sapien
41	367	30.0	106	1	KACB_RAT	P01835 rattus norv
42	367	30.0	108	1	KVJ3H_HUMAN	P01599 homo sapien
43	365	29.8	108	1	KVJ1S_HUMAN	P01611 homo sapien
44	364	29.8	108	1	KVJ1A_HUMAN	P01593 homo sapien
45	364	29.8	108	1	KVJ1Y_HUMAN	P01562 homo sapien

ALIGNMENTS

```

RESULT 1
KVJ1_HUMAN
ID KVJ1_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VG precursor (Fragmen!).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
   within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
-----
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   or send an email to license@isb.slb.ch).
-----
CC EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HVG.
DR HSSP; P80362; 1WT.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006953; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Ilike.
DR InterPro; IPR003006; Ig-MHC.
DR InterPro; IPR003596; Ig-V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115
FT DOMAIN 21 43 IG KAPPA CHAIN V-II REGION VG.
FT DOMAIN 44 54 FRAMEWORK-1.
FT DOMAIN 55 69 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 70 76 FRAMEWORK-2.
FT DOMAIN 77 108 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 109 115 FRAMEWORK-3.
FT DISULFID 43 108 COMPLEMENTARITY-DETERMINING-3.
FT NON_TER 115 115 BY SIMILARITY.
SQ
SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;
Query Match 46.4%; Score 568; DB 1; Length 115;
Best local Similarity 93.9%; Pred. No. 3.1e-41;
Matches 108; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
 |||||
 DB 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
 |||||
 QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDTLTSLISLEPEDFAVYVYCOQRNMP 115
 |||||
 DB 61 GOAPRLIYDASNRATGIPARFSGSGGTDTLTSLISLEPEDFAVYVYCOQRNMP 115
 |||||

RESULT 2

KV3H_HUMAN STANDARD: PRT: 129 AA.
 ID KV3H_HUMAN
 AC P04207;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region CLL precursor (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=68177570; PubMed=3083417;
 RA Jirik F.R., Sarge J., Fong S., Helzmann J.G., Curo J.G., Chen P.P.,
 RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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 CC
 DR EMBL: M12740; AAAS8992.1; -
 DR HSSP: P80362; IWTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_Like: 1.
 DR Immunoglobulin V region: Signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 129 IG KAPPA CHAIN V-II REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JKI SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14275 MW; SC13B411BE60CC14 CRC64;

Query Match 46.1%; Score 563.5; DB 1; Length 129;
 Best Local Similarity 83.7%; Pred. No. 8.5e-41;
 Matches 108; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
 |||||
 DB 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
 |||||
 QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDTLTSLISLEPEDFAVYVYCOQRNMP 115
 |||||

DB 61 GOAPRLIYDTSNRATGIPARFSGSGGTDTLTSLISLEPEDFAVYVYCOQRNMP 115
 |||||
 QY 120 OCTKVEFKR 128
 |||||
 DB 121 OCTKVEIKR 129
 |||||

RESULT 3

KV3M_HUMAN STANDARD: PRT: 129 AA.
 ID KV3M_HUMAN
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=68177307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy."
 RL J. Exp. Med. 167:840-852(1988).
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 CC -----
 CC
 DR PIR: P10021; K3HCHI.
 DR HSSP: P80362; IWTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_Like: 1.
 DR Immunoglobulin V region: Signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 129 IG KAPPA CHAIN V-II REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JKI SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 46.0%; Score 562.5; DB 1; Length 129;
 Best Local Similarity 85.3%; Pred. No. 1e-40;
 Matches 110; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 59
 |||||
 DB 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60
 |||||
 QY 60 GOAPRLIYDTSNRATGIPARFSGSGGTDTLTSLISLEPEDFAVYVYCOQRNMP 115
 |||||
 DB 61 GOAPRLIYDTSNRATGIPARFSGSGGTDTLTSLISLEPEDFAVYVYCOQRNMP 115
 |||||
 QY 120 OCTKVEFKR 128
 |||||
 DB 121 OCTKVEIKR 129
 |||||

RESULT 4	QUERY	SCORE	DB 1	LENGTH	DB 2	LENGTH	DB 3	LENGTH	DB 4	LENGTH	DB 5	LENGTH	DB 6	LENGTH	DB 7	LENGTH	DB 8	LENGTH	DB 9	LENGTH	DB 10	LENGTH	DB 11	LENGTH	DB 12	LENGTH	DB 13	LENGTH	DB 14	LENGTH	DB 15	LENGTH	DB 16	LENGTH	DB 17	LENGTH	DB 18	LENGTH	DB 19	LENGTH	DB 20	LENGTH	DB 21	LENGTH	DB 22	LENGTH	DB 23	LENGTH	DB 24	LENGTH	DB 25	LENGTH	DB 26	LENGTH	DB 27	LENGTH	DB 28	LENGTH	DB 29	LENGTH	DB 30	LENGTH	DB 31	LENGTH	DB 32	LENGTH	DB 33	LENGTH	DB 34	LENGTH	DB 35	LENGTH	DB 36	LENGTH	DB 37	LENGTH	DB 38	LENGTH	DB 39	LENGTH	DB 40	LENGTH	DB 41	LENGTH	DB 42	LENGTH	DB 43	LENGTH	DB 44	LENGTH	DB 45	LENGTH	DB 46	LENGTH	DB 47	LENGTH	DB 48	LENGTH	DB 49	LENGTH	DB 50	LENGTH	DB 51	LENGTH	DB 52	LENGTH	DB 53	LENGTH	DB 54	LENGTH	DB 55	LENGTH	DB 56	LENGTH	DB 57	LENGTH	DB 58	LENGTH	DB 59	LENGTH	DB 60	LENGTH	DB 61	LENGTH	DB 62	LENGTH	DB 63	LENGTH	DB 64	LENGTH	DB 65	LENGTH	DB 66	LENGTH	DB 67	LENGTH	DB 68	LENGTH	DB 69	LENGTH	DB 70	LENGTH	DB 71	LENGTH	DB 72	LENGTH	DB 73	LENGTH	DB 74	LENGTH	DB 75	LENGTH	DB 76	LENGTH	DB 77	LENGTH	DB 78	LENGTH	DB 79	LENGTH	DB 80	LENGTH	DB 81	LENGTH	DB 82	LENGTH	DB 83	LENGTH	DB 84	LENGTH	DB 85	LENGTH	DB 86	LENGTH	DB 87	LENGTH	DB 88	LENGTH	DB 89	LENGTH	DB 90	LENGTH	DB 91	LENGTH	DB 92	LENGTH	DB 93	LENGTH	DB 94	LENGTH	DB 95	LENGTH	DB 96	LENGTH	DB 97	LENGTH	DB 98	LENGTH	DB 99	LENGTH	DB 100	LENGTH	DB 101	LENGTH	DB 102	LENGTH	DB 103	LENGTH	DB 104	LENGTH	DB 105	LENGTH	DB 106	LENGTH	DB 107	LENGTH	DB 108	LENGTH	DB 109	LENGTH	DB 110	LENGTH	DB 111	LENGTH	DB 112	LENGTH	DB 113	LENGTH	DB 114	LENGTH	DB 115	LENGTH	DB 116	LENGTH	DB 117	LENGTH	DB 118	LENGTH	DB 119	LENGTH	DB 120	LENGTH	DB 121	LENGTH	DB 122	LENGTH	DB 123	LENGTH	DB 124	LENGTH	DB 125	LENGTH	DB 126	LENGTH	DB 127	LENGTH	DB 128	LENGTH	DB 129	LENGTH	DB 130	LENGTH	DB 131	LENGTH	DB 132	LENGTH	DB 133	LENGTH	DB 134	LENGTH	DB 135	LENGTH	DB 136	LENGTH	DB 137	LENGTH	DB 138	LENGTH	DB 139	LENGTH	DB 140	LENGTH	DB 141	LENGTH	DB 142	LENGTH	DB 143	LENGTH	DB 144	LENGTH	DB 145	LENGTH	DB 146	LENGTH	DB 147	LENGTH	DB 148	LENGTH	DB 149	LENGTH	DB 150	LENGTH	DB 151	LENGTH	DB 152	LENGTH	DB 153	LENGTH	DB 154	LENGTH	DB 155	LENGTH	DB 156	LENGTH	DB 157	LENGTH	DB 158	LENGTH	DB 159	LENGTH	DB 160	LENGTH	DB 161	LENGTH	DB 162	LENGTH	DB 163	LENGTH	DB 164	LENGTH	DB 165	LENGTH	DB 166	LENGTH	DB 167	LENGTH	DB 168	LENGTH	DB 169	LENGTH	DB 170	LENGTH	DB 171	LENGTH	DB 172	LENGTH	DB 173	LENGTH	DB 174	LENGTH	DB 175	LENGTH	DB 176	LENGTH	DB 177	LENGTH	DB 178	LENGTH	DB 179	LENGTH	DB 180	LENGTH	DB 181	LENGTH	DB 182	LENGTH	DB 183	LENGTH	DB 184	LENGTH	DB 185	LENGTH	DB 186	LENGTH	DB 187	LENGTH	DB 188	LENGTH	DB 189	LENGTH	DB 190	LENGTH	DB 191	LENGTH	DB 192	LENGTH	DB 193	LENGTH	DB 194	LENGTH	DB 195	LENGTH	DB 196	LENGTH	DB 197	LENGTH	DB 198	LENGTH	DB 199	LENGTH	DB 200	LENGTH	DB 201	LENGTH	DB 202	LENGTH	DB 203	LENGTH	DB 204	LENGTH	DB 205	LENGTH	DB 206	LENGTH	DB 207	LENGTH	DB 208	LENGTH	DB 209	LENGTH	DB 210	LENGTH	DB 211	LENGTH	DB 212	LENGTH	DB 213	LENGTH	DB 214	LENGTH	DB 215	LENGTH	DB 216	LENGTH	DB 217	LENGTH	DB 218	LENGTH	DB 219	LENGTH	DB 220	LENGTH	DB 221	LENGTH	DB 222	LENGTH	DB 223	LENGTH	DB 224	LENGTH	DB 225	LENGTH	DB 226	LENGTH	DB 227	LENGTH	DB 228	LENGTH	DB 229	LENGTH	DB 230	LENGTH	DB 231	LENGTH	DB 232
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GN IGCk.
OC Homo sapiens (Human).
OC Euarystia: Metazoa: Chordata: Cranialata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Primates: Catarrhini: Hominoide: Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; Pubmed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Etelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RL acid sequence of the light chain.";
RN Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; Pubmed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL Intrachain disulfide bonds.";
RN Biochemistry 9:3188-3196(1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72188439; Pubmed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RL immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT T1). IV. The complete amino acid sequence and its significance for
RL the mechanism of antibody production.";
RN Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972.).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; Pubmed=6775818;
RA Hietel P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region
RL genes conserve homology in functional segments.";
RN Cell 22:197-207(1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RT Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RN Gamma globulins: structure and function, pp.57-71, Academic Press,
RL New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; Pubmed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RL type).";
RN Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; Pubmed=4893682;
RA Titani K., Shioda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RL complete sequence and the location of the disulfide bridges.";
RN J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; Pubmed=5447531;
RA Konler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RL chains.";
RN Science 169:56-59(1970).
RN [9]
RP SEQUENCE OF 1-33; 38-41 AND 62-80.
RC TISSUE-Abdominal adipose tissue;
RX Pubmed=9588180;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of Al-amyloid protein from abdominal wall,
RL subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RN Biochem. Biophys. Res. Commun. 245:713-716(1998).
RN -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (1,3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC

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CC          MARKER, 45-ALA AND 83-LEU.
CC          -1- SIMILARITY: Contains 1 Immunoglobulin-like domain.
CC          -----
CC          This SWISS-PROT entry is copyright. It is produced through a collaboration
CC          between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC          the European Bioinformatics Institute. There are no restrictions on its
CC          use by non-profit institutions as long as its content is in no way
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CC          entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC          or send an email to license@isb-slb.ch).
CC          -----
DR          EMBL: J00241; AAA58989.1; -.
DR          EMBL: V00557; CA23823.1; -.
DR          PIR: B90562; K3H0.
DR          PDB: 1D5B; 09-FEB-00.
DR          PDB: 1D51; 09-FEB-00.
DR          PDB: 1D6V; 04-OCT-00.
DR          PDB: 1HEZ; 10-AUG-01.
DR          PDB: 1HKL; 12-MAR-97.
DR          PDB: 1I7Z; 08-AUG-01.
DR          PDB: 1M1M; 15-MAY-97.
DR          Genew: HGNC:5716; IGKC.
DR          MIM: 147200; -.
DR          GO: 0003823; F:antigen binding activity; NAS.
DR          GO: 0006955; P:immune response; NAS.
DR          InterPro: IPR007110; Ig-like.
DR          InterPro: IPR003597; Ig-cl.
DR          InterPro: IPR003006; Ig_MHC.
DR          Pfam: PF00047; Ig; 1.
DR          SMART: SM00407; IGH1.1.
DR          PROSITE: PS50835; IG_LIKE; 1.
DR          PROSITE: PS00290; IG_MHC; 1.
DR          Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT          NON_TER 1 102 IG-LIKE.
FT          DOMAIN 5 86
FT          DISULFID 26 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT          VARIANT 83 83 V->L (IN INV(1,2) MARKER).
FT          VARIANT /FTID=VAR.003897.
FT          CONFLICT 14 14 D->N (IN REF. 7 AND 8).
FT          CONFLICT 57 57 E->Q (IN REF. 5 AND 6).
SQ          SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;

Query Match 44.8%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TVAAPSVFIFPPSDEQLKSGTASVCLINFFYPRRAKVKQKVDNALQSGNSQESVTEQDS 188
DB 1 TVAAPSVFIFPPSDEQLKSGTASVCLINFFYPRRAKVKQKVDNALQSGNSQESVTEQDS 60

QY 189 KDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
DB 61 KDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6
KV3K_HUMAN STANDARD; PRT; 128 AA.
ID KV3K_HUMAN
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region IARC/BLA1 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combitato G., Solomon A., Zachau H.G.;
RT "Human Immunoglobulin kappa light chain genes of subgroups II and

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RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC          -----
CC          This SWISS-PROT entry is copyright. It is produced through a collaboration
CC          between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC          the European Bioinformatics Institute. There are no restrictions on its
CC          use by non-profit institutions as long as its content is in no way
CC          modified and this statement is not removed. Usage by and for commercial
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CC          or send an email to license@isb-slb.ch).
CC          -----
DR          EMBL: 200021; CA47316.1; -.
DR          PIR: A01899; K3H041.
DR          HSP: P01607; 1RE1.
DR          GO: 0005576; C:extracellular; NAS.
DR          GO: 0003823; F:antigen binding activity; NAS.
DR          GO: 0006955; P:immune response; NAS.
DR          InterPro: IPR007110; Ig-like.
DR          InterPro: IPR003006; Ig_MHC.
DR          InterPro: IPR003596; Ig_v.
DR          Pfam: PF00047; Ig; 1.
DR          SMART: SM00406; IGH1.1.
DR          PROSITE: PS50835; IG_LIKE; 1.
DR          Immunoglobulin V region; Signal.
FT          SIGNAL 1 20
FT          CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BLA1.
FT          DOMAIN 21 43 FRAMEWORK-1.
FT          DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT          DOMAIN 55 69 FRAMEWORK-2.
FT          DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT          DOMAIN 77 108 FRAMEWORK-3.
FT          DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT          DOMAIN 118 128 JK1 SEGMENT.
FT          DISULFID 43 128 BY SIMILARITY.
FT          NON_TER 128 128
SQ          SEQUENCE 128 AA; 14070 MW; C08957F0EB3B9012 CRC64;

Query Match 43.3%; Score 529; DB 1; Length 128;
Best Local Similarity 81.2%; Pred. No. 6.8e-38;
Matches 104; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 MEAPQQLFLFLMLPDTGTGELVLTQSPATLSLSPGERATLACRASQTSRYLAWQKP 60
DB 1 METPAQLFLFLMLPDTGTGELVLTQSPATLSLSPGERATLACRASQTSRYLAWQKP 60

QY 61 GQAPRLIYDPSNRATGIPARPSGSGDTFLTSLSLEPEFAVYYCQQRNMPWTFQ 120
DB 61 GQSPRLIRDASSRANGIPDRPSGSGDTFLTSLSLEPEFAVYYCQQRSTSPYTFQ 120

QY 121 GTRVEFKR 128
DB 121 GTRKEIKR 128

RESULT 7
KV3J_HUMAN STANDARD; PRT; 116 AA.
ID KV3J_HUMAN
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).

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CC	-----	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	CC
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC	the European Bioinformatics Institute. There are no restrictions on its use by	CC
CC	non-profit institutions as long as their content is in no way	CC	modified and this statement is not removed. Usage by and for commercial	CC
CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/	CC	or send an email to license@isb-sdb.ch).	CC
DR	EMBL; X02725; ?; NOT_ANNOTATED_CDS.	DR		DR
DR	PIR; A01901; K3HUVH.	DR		DR
DR	HSSP; P80362; 1MTL.	DR		DR
DR	GO; GO:0005576; C:extracellular; NAS.	DR		DR
DR	GO; GO:0003823; F:antigen binding activity; NAS.	DR		DR
DR	GO; GO:0006955; P:immune response; NAS.	DR		DR
DR	InterPro; IPR007110; IG_1ike.	DR		DR
DR	InterPro; IPR003006; IG_MHC.	DR		DR
DR	InterPro; IPR003596; IG_V.	DR		DR
DR	Pfam; PF00047; 1g; 1.	DR		DR
DR	SMART; SM00406; IGV; 1.	DR		DR
DR	PROSITE; PS50835; IG_LIKE; 1.	DR		DR
DR	Immunoglobulin V region; Signal.	DR		DR
FT	SIGNAL	FT	1	FT
FT	CHAIN	FT	21	FT
FT	DOMAIN	FT	21	FT
FT	DOMAIN	FT	21	FT
FT	DOMAIN	FT	44	FT
FT	DOMAIN	FT	56	FT
FT	DOMAIN	FT	71	FT
FT	DOMAIN	FT	78	FT
FT	DOMAIN	FT	110	FT
FT	DISULFID	FT	43	FT
FT	NON_TER	FT	116	FT
SQ	SEQUENCE	SQ	116 AA; 12757 MW; 51CD55BA53B21929 CRC64;	SQ
Query Match	40.4%;	Score	494.5;	DB 1;
Match	Local Similarity	83.68;	Pred. No. 4.8e-35;	Length 116;
Matches	97;	Conservative	6;	Mismatches 12;
				Indels 1;
				Gaps 1;
QY	1 MEAPAQQLFLLLLPDTTGEIVLTQSPATLSLSPGERATLACRASOT-ASRYLAWYQK 59			
Db	1 MEAPAQQLFLLLLPDTTTRIVMTQSPITLSLSPGERVTLSCRASQSVSSYLYWYQK 60			
QY	60 PGQAPRLILYDTSNRATGIPARFSGSGSGTDFTLSSISLEPEDFAVYVYQGRFMP 115			
Db	61 PGQAPRLILYDTSNRATGIPARFSGSGSGTDFTLSSISLEPEDFAVYVYQGRFMP 116			
RESULT 8				
KV3B_HUMAN	STANDARD;	PRT;	109 AA.	
AC	P01620;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	1g kappa chain V-II region SIE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=82046598; PubMed=6794615;			
RA	Andrew D.W., Capra J.D.;			
RT	"Antino acid sequence of the variable regions of light chains from two			
RT	idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa			
RT	group."			
RL	Biochemistry 20:5816-5822(1981).			
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA			
CC	GLOBULIN ACTIVITY.			
CC	PIR: A01892; K3HUSI.			
DR	HSSP; P80362; 1MTL.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; NAS.			

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DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Iq_Like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_V.
DR Pfam: PF00047; Iq: 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; Iq_LIKE; 1.
KW Immunoglobulin V region.
DR DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3EC646FEB4 CXC64;
BY SIMILARITY.

Query Match 36.7%; Score 448.5; DB 1; Length 109;
Best Local Similarity 81.7%; Pred. No. 3.4e-31;
Matches 89; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

OY 21 EIVLTQSPATLSISPGERATLACRASQNASR-YLAWYQKPGQAPRLLIYDTSNRAQIP 79
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1 EIVLTQSGTSLISPGERATLISCRASQSVNSYSLAWYQKPGQAPRLLIYGASSRAQIP 60
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 80 ARFGSGSGDTFTLISISLEPEDFAVYCCQGRFNMPWFGJGTKEFKR 128
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 61 DRFGSGSGDTFTLISLRLEDDRAVYCCQYGGSSPQIFGSKVEIKR 109
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 9
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Iq kappa chain V-II region Tl.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE.
RX MEDLINE:72188439; PubMed:5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
   "Rule of antibody structure. The primary structure of a monoclonal
   immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
   T1). IV. The complete amino acid sequence and its significance for
   the mechanism of antibody production.";
   Hoppe-Seivier's Z. physiol. Chem. 353:189-208(1972).
RL -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
CC PIR: A01895; K3HUT1.
DR HSSP: P80362; 1MTL.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Iq_Like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_V.
DR Pfam: PF00047; Iq: 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; Iq_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
DR DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CC6C7749BC CXC64;

Query Match 36.7%; Score 448.5; DB 1; Length 109;
Best Local Similarity 82.6%; Pred. No. 3.4e-31;
Matches 90; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

OY 21 EIVLTQSPATLSISPGERATLACRASQNASR-YLAWYQKPGQAPRLLIYDTSNRAQIP 79
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1 EIVLTQSGTSLISPGERATLISCRASQSVNSYSLAWYQKPGQAPRLLIYGASSRAQIP 60
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY 80 ARFGSGSGDTFTLISISLEPEDFAVYCCQGRFNMPWFGJGTKEFKR 128
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 61 DRFGSGSGDTFTLISLRLEDDRAVYCCQYGGSSPQIFGSKVEIKR 109
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

80 ARFGSGSGDTFTLISISLEPEDFAVYCCQGRFNMPWFGJGTKEFKR 128

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CC CC Biochemistry 20:5816-5822(1981)).
DR -I- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-CAMMA
DR GLOBULIN ACTIVITY.
DR PIR; A01896; K3HOWL.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPRO03596; Ig_v.
DR SMART; SMO0406; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DISULEFD 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 36.1%; Score 441.5; DB 1; Length 109;
Best Local Similarity 81.7%; Pred. No. 1,3e-30;
Matches 89; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

QY 21 EIVLTGSPATLSIPGERATLACRASOT-ASRYLAHWQQKPGQAPELLIDTSNRAGIP 79
Db 1 EIVLTGSPGLTSLISPGERATLSCRASGVSGYLGHVQQKPPGAPELLITIGASSRATGIP 60
QY 80 ARFGSGGGSDFTFLSLSLEPEDFAVVYYCOQRFNWPPTFGQGTRKEPKR 128
Db 61 DRFSGSGGGTDFLTLLTISRLEDPAVVYYCQGYSLGRTPFGQTRVEIKR 109

RESULT 12
KV3G_HUMAN STANDARD; PRT; 109 AA.
AC ID KV3G_HUMAN P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DE Ig kappa chain V-IIJ region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX OX NCBI_TaxID=9606;
RN [1]
RP RP MEDLINE=68230578; PubMed=3086710;
RX RX Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with anti-peptide antibodies.";
RL RL Mol. Immunol. 23:239-244(1986).
DR DR PIR; A01893; K3HUGO.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:Immune response; NAS.
DR InterPro; IPRO07110; Ig-like.
DR InterPro; IPRO03006; Ig_MHC.
DR InterPro; IPRO03596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KM KM Immunoglobulin V region.
FT DISULEFD 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5BD93588B6 CRC64;

Query Match 36.1%; Score 441.5; DB 1; Length 109;
Best Local Similarity 80.7%; Pred. No. 1,3e-30;
Matches 88; Conservative 8; Mismatches 12; Indels 1; Gaps 1;
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
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CC EMBL: 20020; CAA77315.1; .
CC PIR: A01890; K2HURP.
CC HSSP: P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPM1 6410.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CAFA3673009EE CRC64;

Query Match 35.0%; Score 427.5; DB 1; Length 133;
Best Local Similarity 58.6%; Pred. No. 2.5e-29;
Matches 78; Conservative 24; Mismatches 26; Indels 5; Gaps 1;

OY 1 MEAPALFLFLMLPDTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MRLPAQLGLMLMWPGSSGDVVMQPSLPLVTLGPASISCRSSQSLIVSDGNTYLLNW 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 56 YQAKPGQAPRLLIYTSNRATGIPARFSGSGSGTDFTLSSISLEPEDFAVYYCQGRFNP 115
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 FQQRPGQSPRRILYVNSRDGVPDREFSGSGGTDFTLKISRVEADYGVYYCMQGTWMS 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 116 WTFGGTKVEFKR 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 WTFGGTKVEIKR 133
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: September 12, 2003, 13:01:16
Job time : 10.9153 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:57:09 ; Search time 17.5169 seconds
(without alignments)
1284.668 Million cell updates/sec

Title: US-09-848-832-4

Perfect score: 1223

Sequence: 1 MEAPAQLFLILLMLPDRTG.....EVTHQGLSSPYTKSFNRGEC 234

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.76:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1010.5	82.6	215	2 JE0242	Ig kappa chain NIG
2	983.5	80.4	215	2 JE0244	Ig kappa chain NIG
3	971.5	79.4	215	2 JE0243	Ig kappa chain NIG
4	944.5	77.2	215	2 A23746	Ig kappa chain V-I
5	848	69.3	216	2 JE0241	Ig kappa chain Am3
6	771	63.0	240	2 S06084	Ig kappa chain pre
7	727	58.4	234	2 S01320	Ig kappa chain pre
8	717	58.6	234	2 S14237	Ig kappa chain pre
9	703.5	57.5	230	2 S31161	Ig kappa chain - s
10	702.5	57.4	219	2 S38865	Ig kappa chain - m
11	702.5	57.4	225	2 S37484	Ig kappa chain - m
12	702	57.4	218	2 S68241	Ig kappa chain V r
13	696	56.9	218	2 JCS810	Ig kappa chain V r
14	695	56.8	144	2 PLO106	Ig kappa chain pre
15	695	56.8	220	2 A31790	Ig kappa chain V r
16	692.5	56.6	235	2 S25058	Ig kappa chain - m
17	681.5	55.7	219	2 PC4203	Ig kappa chain (no
18	681.5	55.7	219	2 S52028	Ig kappa chain - m
19	678.5	55.5	225	2 JLO029	Ig kappa chain pre
20	677.5	55.4	217	2 S42772	Ig kappa chain - m
21	673.5	55.1	214	2 S16112	Ig kappa chain V r
22	672	54.9	214	2 S68212	Ig kappa chain (Ma
23	667	54.5	210	2 A56169	Ig kappa chain V r
24	613.5	50.2	135	2 S52059	Ig kappa chain V r
25	610	49.9	178	2 PTO219	Ig kappa chain V-C
26	609	49.8	128	2 S40379	Ig kappa chain V-J
27	600	49.1	128	2 A56701	Ig kappa chain V r
28	588.5	48.1	145	2 S20631	Ig kappa chain - h
29	584	47.8	125	2 S40344	Ig kappa chain V-J

30	582	47.6	129	2 S29627	Ig kappa chain V r
31	575.5	47.1	197	2 S29593	Ig kappa chain (W)
32	569	46.5	128	2 S40345	Ig kappa chain V-J
33	568	46.4	115	1 K3HVG	Ig kappa chain pre
34	565	46.2	128	2 S40343	Ig kappa chain V-J
35	563.5	46.1	229	2 A20969	Ig kappa chain pre
36	562.5	46.0	129	1 K3HUI	Ig kappa chain pre
37	562.5	46.0	129	2 S40363	Ig kappa chain - h
38	553.5	45.3	129	1 K3HUA	Ig kappa chain pre
39	552.5	45.2	129	1 S49532	Ig kappa chain V
40	548	44.8	106	1 K3HU	Ig kappa chain C r
41	547.5	44.8	128	2 S20636	Ig kappa chain V r
42	546.5	44.7	238	2 A49633	Ig lambda-like cha
43	545	44.6	111	2 S23628	Ig kappa chain V r
44	545	44.6	115	2 S11697	Ig kappa chain pre
45	544.5	44.5	131	2 S40328	Ig kappa chain - h

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C/Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis:

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

F:16-91/Domain: Immunoglobulin homology <IMV>

Query Match 82.6%; Score 1010.5; DB 2; Length 215;

Best Local Similarity 91.6%; Pred. No. 1.1e-62;

Matches 197; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

OY	21	EVLTGSPATLSLSPGERATLACRASQTS-RLAWYQOKPGQAPRLIYDTSNRATGIP 79	
DB	1	EIVLTGSPPTLSLSPERATLSRASQSVNNILAWYQOKPGQAPRLIYDASSRATGIP 60	
OY	80	ARFSGSGSTDFLTLSISLEPEDFAVYQCQRFNWPMTFGJGTRVEFKRTVAAPSVFIRP 139	
DB	61	DRFSGSGSTDFLTLSISLEPEDFAVYCCQYDRPMTFGJGTRVEIKRTVAAPSVFIRP 120	
OY	140	PSDEOLKSGTASVCLNNFYPREAKVQKVDNALDSGNSDESVTEDSKDSTYSLSSTL 199	
DB	121	PSDEOLKSGTASVCLNNFYPREAKVQKVDNALDSGNSDESVTEDSKDSTYSLSSTL 180	
OY	200	TLSKADYEKKHYACEVTHQGLSSPYTKSFNRGEC 234	
DB	181	TLSKADYEKKHYACEVTHQGLSSPYTKSFNRGEC 215	

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C/Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yanagata, F.; Yamaki, S.; Kazi, H.

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VK) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

F:16-90/Domain: Immunoglobulin homology <IMV>

Query Match	80.44;	Score 983.5;	DB 2;	Length 215;
Best Local Similarity	89.34;	Pred. No. 7,66-61;		
Matches 192;	Conservative 7;	Mismatches 15;	Indels 1;	Gaps 1;
QY	21	EIVLTGSPATLSLSPGERATLACRASQTASHRYLAWYQKPGQAPRRLIYDTSNRATGIPA	80	
	1	EVLTGSPATLSVSPGERATLSCRASQSYHSLNLAWYQKPGQAPRRLIYRASTRATGIPA	60	
Db				
QY	81	RFSSSGSGTDFTLSSISLEPEDFAVYVCOQRENN - PMTFGGGTKEVKRRYVAADSVFIIP	139	
	61	RFSSSGSGTDFILTISSLOSSEDFALYVCOQYNTMPPLTFGGGTKEVKRVAAPSVFIIP	120	
Db				
QY	140	PSDQLKSGTASYVCLLNFFYPRAKQVQKVDNALQSGNSQSEVTEEDDSKDTSTLSSTL	199	
	121	PSDQLKSGTASYVCLLNFFYPRAKQVQKVDNALQSGNSQSEVTEEDDSKDTSTLSSTL	180	
Db				
QY	200	TLSKADYEKKRVYACEVTHQGLSSPVTKSFNRGEC	234	
	181	TLSKADYEKKRVYACEVTHQGLSSPVTKSFNRGEC	215	
Db				

```

RESULT 3
JE0243
Ig kappa chain NIG93 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0243
R:Alim, M.A.; Hata, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
A/Accession: JE0243
A:Molecule_type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:/16-90/Domain: immunoglobulin homology <IMX>

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RESULT 4
A23746
I: kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
J:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2835-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A:Reference number: A23746; PMID:9131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>

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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match	77.2%	Score 944.5	DB 2	Length 215
Best Local Similarity	89.7%	Pred. No. 3,6e-58		
Matches	192	Conservative	6	Mismatches 15; Indels 1; Gaps 1
QY	21	EIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQOQPCGAPRLITYDTSNRRATGIP	79	
DB	1	EIVLTQSPATLSLSPGERATLSGASVSSNYLAWYQOQPCGAPRLITYDTSNRRATGIP	60	
QY	80	ARFSSGSGSTDITLISLLEPDPFVYVYQOQRFNMPWTFPGCGTKVEFKRTVAAPSVFIRP	139	
DB	61	DRFSSGSGSTDITLISLLEPDPFVYVYQOQSGSPDLTGGGKTKEIKRTVAAPSVFIRP	120	
QY	140	PSDEGLKGTASVYCLLNLFYPREAKVQWRYNALQSGNSQSVTFEODSKDSTYSLSFTL	199	
DB	121	PSDEGLKGTASVYCLLNLFYPREAKVQWRYNALQSGNSQSVTFEODSKDSTYSLSFTL	180	
QY	200	TLSKADYEKKHVVACEVTHQGLSSPVTKSFNNGE	233	
DB	181	TLSKADYEKKHVVAGEVTHQGLSSPVTKSFNNGE	214	

RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPII, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALT>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain c
A:Reference number: S06084; MUID:90016888; PMID:2508067
Accession: S06084

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OM protein - protein search, using sw model

Run on: September 12, 2003, 13:00:49 ; Search time 30.7966 Seconds
(without alignments)
2245.783 Million cell updates/sec

Title: US-09-848-832-3
Perfect score: 2514
Sequence: 1 MEFGSLWFLVAILKGVOCE.....MHEALHNHYTKSLSPGK 474

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCRT_NEM_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEM_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCRTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	2514	100.0	474	12	US-10-225-108A-3	Sequence 3, Appl1
2	2514	100.0	474	12	US-09-848-832-3	Sequence 3, Appl1
3	2279	90.7	449	10	US-09-736-371B-21	Sequence 21, Appl1
4	2257	89.8	451	10	US-09-832-698A-26	Sequence 26, Appl1
5	2249	89.5	444	15	US-10-150-475A-6	Sequence 6, Appl1
6	2196	87.4	470	15	US-10-020-786-9	Sequence 9, Appl1
7	2196	87.4	470	15	US-10-227-694-5	Sequence 5, Appl1
8	2193.5	87.3	452	11	US-09-726-258-71	Sequence 71, Appl1
9	2187	87.0	476	15	US-10-020-786-11	Sequence 11, Appl1
10	2183	86.8	478	10	US-09-948-429B-8	Sequence 8, Appl1
11	2183	86.8	478	12	US-10-124-807-8	Sequence 8, Appl1
12	2183	86.8	478	14	US-10-124-805-8	Sequence 8, Appl1
13	2181.5	86.8	449	12	US-10-356-974-2	Sequence 2, Appl1
14	2181.5	86.8	449	15	US-10-253-366-2	Sequence 2, Appl1
15	2181.5	86.8	449	15	US-10-316-694-2	Sequence 2, Appl1

16	2178	86.6	453	9	US-09-802-077-8	Sequence 8, Appl1
17	2178	86.6	453	9	US-09-802-096-8	Sequence 8, Appl1
18	2178	86.6	453	11	US-09-925-179-8	Sequence 18, Appl1
19	2173	86.4	451	9	US-09-920-171-18	Sequence 18, Appl1
20	2173	86.4	451	12	US-10-113-996-18	Sequence 18, Appl1
21	2173	86.4	451	12	US-10-292-869-2	Sequence 2, Appl1
22	2173	86.4	451	12	US-09-792-938-2	Sequence 3, Appl1
23	2171.5	86.4	463	15	US-10-153-382-3	Sequence 14, Appl1
24	2170	86.3	451	9	US-09-920-171-14	Sequence 16, Appl1
25	2170	86.3	451	11	US-09-920-171-16	Sequence 65, Appl1
26	2170	86.3	451	11	US-09-925-179-65	Sequence 14, Appl1
27	2170	86.3	451	12	US-10-113-996-14	Sequence 16, Appl1
28	2170	86.3	451	12	US-10-113-996-16	Sequence 9, Appl1
29	2170	86.3	464	15	US-10-153-382-9	Sequence 13, Appl1
30	2168.5	86.3	463	15	US-10-153-382-13	Sequence 66, Appl1
31	2167	86.2	451	11	US-09-925-179-66	Sequence 5, Appl1
32	2165.5	86.1	463	15	US-10-153-382-5	Sequence 68, Appl1
33	2161	86.0	451	11	US-09-925-179-68	Sequence 32, Appl1
34	2159	85.9	470	10	US-09-859-053-32	Sequence 36, Appl1
35	2157	85.8	470	10	US-09-859-053-36	Sequence 157, Appl1
36	2145	85.3	470	15	US-10-216-484-157	Sequence 147, Appl1
37	2134	84.9	470	15	US-10-216-484-147	Sequence 46, Appl1
38	2133.5	84.9	731	10	US-09-825-012-46	Sequence 55, Appl1
39	2133.5	84.9	741	10	US-09-825-012-55	Sequence 143, Appl1
40	2133	84.8	470	15	US-10-216-484-145	Sequence 52, Appl1
41	2131	84.8	470	15	US-10-216-484-143	Sequence 61, Appl1
42	2128.5	84.7	729	10	US-09-825-012-52	Sequence 117, Appl1
43	2128.5	84.7	739	10	US-09-825-012-51	Sequence 41, Appl1
44	2128	84.6	470	15	US-10-216-484-117	
45	2125.5	84.5	467	15	US-10-171-452A-41	

ALIGNMENTS

RESULT 1									
US-10-225-108A-3									
Sequence 3, Application US/10225108A									
Publication NO. US20030157112A1									
GENERAL INFORMATION:									
APPLICANT: HOOVER, Craig									
TITLE OF INVENTION: Recombinant Antibodies, and Compositions									
TITLE OF INVENTION: Recombinant Antibodies, and Compositions									
FILE REFERENCE: 8321-110									
CURRENT APPLICATION NUMBER: US/10/225,108A									
CURRENT FILING DATE: 2003-04-10									
PRIOR APPLICATION NUMBER: US 09/848,832									
PRIOR FILING DATE: 2001-05-04									
PRIOR APPLICATION NUMBER: US 60/204,518									
PRIOR FILING DATE: 2001-05-16									
PRIOR APPLICATION NUMBER: US 60/314,023									
PRIOR FILING DATE: 2001-08-21									
NUMBER OF SEQ ID NOS: 16									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 3									
LENGTH: 474									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-10-225-108A-3									
Query Match									
Best Local Similarity 100.0%; Score 2514; DB 12; Length 474;									
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MEFGSLWFLVAILKGVOCEVOLLSSGGGLVPGGSLRLSFAASGFTFSNVMSVWVROAP	60						
DB	1	MEFGSLWFLVAILKGVOCEVOLLSSGGGLVPGGSLRLSFAASGFTFSNVMSVWVROAP	60						
QY	61	GKGLWEVAISASGSHSTYLAOSVKGRFTISRDNSKNTLYLQNSLRADFTAVYCAKRE	120						
DB	61	GKGLWEVAISASGSHSTYLAOSVKGRFTISRDNSKNTLYLQNSLRADFTAVYCAKRE	120						

QY	121	VTMTVVLVNGCFPYWMOGFRVTVYSSASTKCRPSVFLPRLAPSSKSTVSGTAAALGCLYKDYPRP	180
Db	121	VTMTVVLVNGGFPYWMOGFRVTVYSSASTKCRPSVFLPRLAPSSKSTVSGTAAALGCLYKDYPRP	180
QY	181	VTVSNSGALTVSGVHTFPVALOSSGLYSLSSVTVYVSSLSGQTYICNNHRSNTRKYDK	240
Db	181	VTVSNSGALTVSGVHTFPVALOSSGLYSLSSVTVYVSSLSGQTYICNNHRSNTRKYDK	240
QY	241	RVEPRKCDKTHTCPCPCPAPABELLGCSVFLFPEPKPKDTLMIISRTPEYTCVYVDVSHDEPEY	300
Db	241	RVEPRKCDKTHTCPCPCPAPABELLGCSVFLFPEPKPKDTLMIISRTPEYTCVYVDVSHDEPEY	300
QY	301	KFNMYVDGEVYHNAKTKPREQYNSTYRVVSVLYLHODMLNGEKYCKVSNKALPAPTE	360
Db	301	KFNMYVDGEVYHNAKTKPREQYNSTYRVVSVLYLHODMLNGEKYCKVSNKALPAPTE	360
QY	361	KTISAKAKQPRPQVYTYLPPSRREEMTKNOVSLTCLYKGYPSDIAVEMESNGOPENNYKT	420
Db	361	KTISAKAKQPRPQVYTYLPPSRREEMTKNOVSLTCLYKGYPSDIAVEMESNGOPENNYKT	420
QY	421	TRPVYDSDGSEFLYSLKYVDKSRMOOGANFSCSVNHEALHNHYTQKSLSLSPK	474
Db	421	TRPVYDSDGSEFLYSLKYVDKSRMOOGANFSCSVNHEALHNHYTQKSLSLSPK	474

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RESULT 2
US-09-848-832-3
; Sequence 3, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
; APPLICANT: Hoeper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
; FILE REFERENCE: H0001.NP0002
; CURRENT APPLICATION NUMBER: US/09/848, 832
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/204, 518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 474
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-848-832-3

Query Match          100.0%; Score 2514; DB 12; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.4e-165;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MEFGLSMFLVAILKGVOCCEVOLLBSGGGLVOPGSLRLSCAASGFTFSNYSAMSWRQAP 60
DB      1  MEFGLSMFLVAILKGVOCCEVOLLBSGGGLVOPGSLRLSCAASGFTFSNYSAMSWRQAP 60

QY      61  GKGLEWVAISASGSHSTYLADSVKGFRTISRDNKNTLYLQNMSLRAEDTAAVYYCAADRE 120
DB      61  GKGLEWVAISASGSHSTYLADSVKGFRTISRDNKNTLYLQNMSLRAEDTAAVYYCAADRE 120

QY      121  VTMIIVLNGGFDYWGQGTFRVTVSSASTKGPVSEFLPLPSSKSTSGCTAALGCLVKDYRPEP 180
DB      121  VTMIIVLNGGFDYWGQGTFRVTVSSASTKGPVSEFLPLPSSKSTSGCTAALGCLVKDYRPEP 180

QY      181  VTVSMNAGALNSGVTTFPRAVLQSSGLYSLSVYTVVSSLSIGTQTYICNNHAKPSNTRYDK 240
DB      181  VTVSMNAGALNSGVTTFPRAVLQSSGLYSLSVYTVVSSLSIGTQTYICNNHAKPSNTRYDK 240

QY      241  RVEPKSCDKTHTCCPCPAPELLGSPVFLFPPKPKDTLMISRPETVCVVVDVSHEDPEV 300
DB      241  RVEPKSCDKTHTCCPCPAPELLGSPVFLFPPKPKDTLMISRPETVCVVVDVSHEDPEV 300

QY      301  KFNRYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEVCKVNALPAPIE 360
DB      301  KFNRYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEVCKVNALPAPIE 360

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Db	301	KFNMYVDGVEYNNATKPRPEEYNSIYRVAVSLYTLHODMLNGKEKCKAYSKNALPAPIE	360
QY	361	KTISAKGCPREPPQYITLPPREEMTKKNVSLTCLYKGYPSDIAYEWESNGPENNYKT	420
Db	361	KTISAKGCPREPPQYITLPPREEMTKKNVSLTCLYKGYPSDIAYEWESNGPENNYKT	420
QY	421	TPPYLDSDGSEFLYLSKLTVDKSRMOGNAVFSCSVMEALHNHYTQKSLSLSPCK	474
Db	421	TPPYLDSDGSEFLYLSKLTVDKSRMOGNAVFSCSVMEALHNHYTQKSLSLSPCK	474

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RESULT 3
US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736,371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-371B-21

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[illegible]

[illegible]

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RESULT 7
US-10-227-694-5
: Sequence 5, Application US/10227694
: Publication No. US20030077739A1
: GENERAL INFORMATION:
: APPLICANT: Simmons, Laura
: APPLICANT: Andersen, Dana
: TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
: FILE REFERENCE: P186781
: CURRENT APPLICATION NUMBER: US/10/227,694
: CURRENT FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: US 60/315,209
: PRIOR FILING DATE: 2001-08-27
: NUMBER OF SEQ ID NOS: 6
: SEQ ID NO 5
: LENGTH: 470
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Synthetic
US-10-227-694-5

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Query Match	87.48;	Score 2196;	DB 15;	Length 470;
Best Local Similarity	88.68;	Pred. No. 2.6e-143;		
Matches 418; Conservative	9;	Mismatches 37;	Indels 8;	Gaps 1;

[illegible]

Db	179	VSNNSGALISGVHTFAVVLQSSGKLSSSVTVVPSSSLGTOYICNHNHKSNTKVDKV	238
Oy	243	EPKSCDKHTPCPCAPAPELLGGSVFLPPPKKDFLMSIRPEYTCVVDVSHEDPEYK	3020
Db	239.	EPKSCDKHTPCPCAPAPELLGGSVFLPPPKKDFLMSIRPEYTCVVDVSHEDPEYK	2989
Oy	303	NWVYDGEVHNATKTRREOYNSTRVYSLVTLVHQDLNCKEYCKKSNKALPAPLEKT	3622
Db	299	NWVYDGEVHNATKTRREOYNSTRVYSLVTLVHQDLNCKEYCKKSNKALPAPLEKT	3586
Oy	363	ISRAKQGPPEPOYYTLPPSRDEMTKNQVSLTCLVKGYPSPDAVEMESNGOPENNYKTPP	4222
Db	359	ISRAKQGPPEPOYYTLPPSRDEMTKNQVSLTCLVKGYPSPDAVEMESNGOPENNYKTPP	4181
Oy	423	PVLDSGGSFPLYSLKLVNDKSRMOOGVPSCSYMHALNNHTQSLSLSPCK	474
Db	419	PVLDSGGSFPLYSLKLVNDKSRMOOGVPSCSYMHALNNHTQSLSLSPCK	470

RESULT 8
US-09-726-258-71
; Sequence 71, Application US/09726258
; Publication No. US20030021790A1

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1 STREET: 1 DNA Way
2 CITY: South San Francisco
3 STATE: California
4 COUNTRY: USA
5 ZIP: 94080
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
9 COMPILER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Mupatin (Genentech)
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/09/726,258
15
16 FILING DATE:
17 CLASSIFICATION:
18
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 09/234,182
21
22 FILING DATE:
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 60/094003
26
27 FILING DATE: 24-JUL-1998
28
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Love, Richard B.
31 REGISTRATION NUMBER: 34,659
32 REFERENCE/DOCKET NUMBER: P1085N4-1A
33
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 650/225-5530
36
37 TELEFAX: 650/952-9881
38
39 INFORMATION FOR SEQ ID NO: 71:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 453 amino acids
42 TYPE: Amino acid
43 TOPOLOGY: Linear
44
45 US-09-726-258-71

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Query Match	87.3%	Score 2193.5	DB 11	Length 452
Best Local Similarly	91.28%	Pred. No. 3.7e-143		
Matches 417; Conservative	9;	Mismatches 24;	Indels 7;	Gaps 2;

[illegible]

Query Match	86.8%	Score 2183;	DB 10;	Length 478;
Best Local Similarity	86.7%;	Pred. No. 2,1e-142;		
Matches 418;	Conservative 18;	Mismatches 34;	Indels 12;	Gaps 3.
Oy	1 MERGLSNLFLVAIIKGVQCEVQLLESGGGLVPPGGSLRL;CAASGFTFSNAMSVMWRAP 60			

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01 M6MSLLELVANATRVGCEVLVESSGGLVQPGCGLRVCAGVSGFTESDHYMMWFRAP 60
02 1 M6MSLLELVANATRVGCEVLVESSGGLVQPGCGLRVCAGVSGFTESDHYMMWFRAP 60
03 61 GGGLEVVSAI--SASHSTYLDASVKGRFTISRDNKNLTLYLOMNSLAEDTAVYYCAKD 118
04 61 GGPPEVVGFIIRNKPNGGTTEYAASVXDRFTISRDSKSIAYLOWSSSLKIEDTAVYYCT-- 118
05 119 RETMTIVLVNG-----FDYWGQGTAVTVSSASTKGPSVFPLAPSSKSTSGTGTAALGCL 172
06 119 --TSYISHRGVCYCIGYFEFWMQOGALVTYSSASTKGPSVFPLPSPSKSIGTRALGCL 176
07 173 VKDYEPETVSNNSGALTISGVHTFPVALIOSSGLYSLSVTVYESSLGITGYICNVNHK 232
08 177 VVDYEPETVSNNSGALTISGVHTFPVALIOSSGLYSLSVTVYESSLGITGYICNVNHK 236
09 223 PSNTKYDKRAEPRSCCKTHCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVD 292
10 237 PSNTKYDKRAEPRSCCKTHCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVD 296
11 293 VSHDEPEVFNMYVDGEVHNNAKTKEPREQYNSTRYVSVLTVAHQDLNKKKEYCKAKYSN 352
12 297 VSHDEPEVFNMYVDGEVHNNAKTKEPREQYNSTRYVSVLTVAHQDLNKKKEYCKAKYSN 356
13 353 KALPAIEKTISSAKQPREPOVYTLPPSRHEEMTKNOVSLTCLVKGTPSDIAVWEWSNG 412
14 357 KALPAIEKTISSAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGTPSDIAVWEWSNG 416
15 413 QENNNKTTTPVLDSDGSFFLYSKLVADKSRRMOOGNFSCSYMHAEALHNYHTOKSLDSP 472
16 417 QENNNKTTTPVLDSDGSFFLYSKLVADKSRRMOOGNFSCSYMHAEALHNYHTOKSLDSP 476
17 473 GK 474
18 477 GK 478
19 RESULT 11
20 US-10-124-807-8
21 ; Sequence 8, Application US/10124807
22 ; Publication No. US20030166207A1
23 ; GENERAL INFORMATION:
24 ; APPLICANT: Anderson, Darrell R.
25 ; TITLE OF INVENTION: "MONKEY MONOCOLONAL ANTIBODIES SPECIFIC
26 ; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
27 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
28 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS."
29 ; NUMBER OF SEQUENCES: 12
30 ; CORRESPONDENCE ADDRESS:
31 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
32 ; STREET: 699 Prince Street
33 ; CITY: Alexandria
34 ; STATE: VA
35 ; COUNTRY: USA
36 ; ZIP: 22314
37 ; COMPUTER READABLE FORM:
38 ; MEDIUM TYPE: Floppy disk
39 ; COMPUTER: IBM PC compatible
40 ; OPERATING SYSTEM: PC-DOS/MS-DOS
41 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
42 ; CURRENT APPLICATION DATA:
43 ; APPLICATION NUMBER: US/10/124, 807
44 ; FILING DATE:
45 ; CLASSIFICATION:
46 ; PRIOR APPLICATION DATA:
47 ; APPLICATION NUMBER: 09/383, 916
48 ; FILING DATE:
49 ; APPLICATION NUMBER: US 08/487, 550
50 ; FILING DATE: 07-JUN-1995
51 ; ATTORNEY/AGENT INFORMATION:
52 ; NAME: Teskin, Robin L.
53 ; REGISTRATION NUMBER: 35,030
54 ; REFERENCE/DOCKET NUMBER: 012712-131
55 ; TELECOMMUNICATION INFORMATION:

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: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 478 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-10-124-807-8

Query Match      86.8%; Score 2183; DB 12; Length 478;
Best Local Similarity 86.7%; Pred. No. 2,1e-142;
Matches 418; Conservative 18; Mismatches 34; Indels 12; Gaps 3;

OY 1 MEGLSLMFLPVALIKGVOCEVOILLSEGGIVQGGSLRLSCAASGFTFSPNWSWRAP 60
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MGSLLILFLPVAATRKQCEVQLVESGGGLVPGGSLRVCASGFTTFSDHMYWFRAP 60
OY 61 GKGLEWYSAI--SASGSHYLAADVSGKRTISDNRKNLTLQMNLSRAEDTAVYYCAKD 118
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 GKGLEWYGFIRNKPNGGTETRYAASVKDRFTISRDSKSIAYLQMSSLKIEDTAVYYCT-- 118
OY 119 REVMYIVLVNGG-----FDYNGQGRVYVSSASTGSPVFLPAPSKSTSGCTAALGCL 172
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 119 --TSYISHCRGGVCGYGGFFEFWQGLVTVYSSASTGSPVFLPAPSKSTSGCTAALGCL 176
OY 173 VKDFPEPPVYVSNMNGSLTSGVHTFPVALQSSGLYLSLSSVYTPSSSLTQTYICNVNHK 232
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 177 VKDFPEPPVYVSNMNGSLTSGVHTFPVALQSSGLYLSLSSVYTPSSSLTQTYICNVNHK 236
OY 233 PSNTKVDKRVKPSKCDTHTCPPCAPABELIGSPVFLPFPKPKDMLISRPEVTCVVD 292
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 237 PSNTKVDKRVKPSKCDTHTCPPCAPABELIGSPVFLPFPKPKDMLISRPEVTCVVD 296
OY 293 VSHEDPEVKNWYVDGEVHNATKPREQYNSTYRVYSVLTVLHODMLNGEKYCKVSN 352
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 297 VSHEDPEVKNWYVDGEVHNATKPREQYNSTYRVYSVLTVLHODMLNGEKYCKVSN 356
OY 353 KALPAPIEKTISRKAGQPREPQYVTLPPSHHEMTKNQVSLTCLVKGFPSDIAVEMESNG 412
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 357 KALPAPIEKTISRKAGQPREPQYVTLPPSHDELTKNQVSLTCLVKGFPSDIAVEMESNG 416
OY 413 OPENNYTTPPEVLDSQSFELYSKLVNDSRMQGGVWFSCVNHKALHHYTKSLSLSP 472
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 417 OPENNYTTPPEVLDSQSFELYSKLVNDSRMQGGVWFSCVNHKALHHYTKSLSLSP 476
OY 473 GK 474
   ||
DB 477 GK 478

RESULT 12
US-10-124-905-8
: Sequence 8, Application US/10124905
: Publication No. US2002016136A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Darrell R.
: TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
: TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
: TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-124-905-8

Query Match      86.8%; Score 2183; DB 14; Length 478;
Best Local Similarity 86.7%; Pred. No. 2,1e-142;
Matches 418; Conservative 18; Mismatches 34; Indels 12; Gaps 3;

Oy 1 MEFGLSMFLVAIIKVOCEVOLLESGGGLVOPGGSLRLSCAASGFTFSNYAMSVMWRQAP 60
Db 1 MGLMILLFLVAIVATRVQCEVOLVESGGGLVOPGGSLRLSCAVSFTSDHMYMFRQAP 60
Oy 61 GKGLEWVAI--SASGHSYVLADSVKGRFTISRDNKMTLYLQNMNLSRAEDTAVYYCAK 118
Db 61 GKGEWVGFIRNKPNGCTTEYAASVDRFTISRDNKSIAYLQMSLSLKIEDTAVYYCT-- 118
Oy 119 REVMIIVLVNG-----FDYWGQGTRTVVSASATKGPSVFPLAASSKSTSGCTAAAGL 172
Db 119 --TSTISHRGVVCYGYFERWGGALVTVSSASTKGPSVFPLAASSKSTSGCTAAAGL 176
Oy 173 VKDYFPEPVTVSMNSGALTSGVHPFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHK 232
Db 177 VKDYFPEPVTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHK 236
Oy 233 PSNTRKVDKRVKSCDKTHTCPCPAPPELLGGPSVFLPPTPKKDTLMIISRTPEVTCVVD 292
Db 237 PSNTRKVDKAEPRKSCDKTHTCPCPAPPELLGGPSVFLPPTPKKDTLMIISRTPEVTCVVD 296
Oy 293 VSHEDPEVKFMWYDGVENVNAKTRPREQYNSTYRVYSVLTVLDHQMILNGEKYCKYSN 352
Db 297 VSHEDPEVKFMWYDGVENVNAKTRPREQYNSTYRVYSVLTVLDHQMILNGEKYCKYSN 356
Oy 353 KALPAPIKTSKAKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEMESNG 412
Db 357 KALPAPIKTSKAKGQPREPOVYTLPPSRREDELTKNQVSLTCLVKGFYPSDIAVEMESNG 416
Oy 413 OPENNYKTTTPVLDSGSEFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSP 472
Db 417 OPENNYKTTTPVLDSGSEFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSP 476
Oy 473 GK 474
Db 477 GK 478

RESULT 13
US-10-356-974-2
; Sequence 2, Application US/10356974
; Publication No. US20030153735A1
; GENERAL INFORMATION:
; APPLICANT: BRECE, TIMOTHY N.
; APPLICANT: FAHRNER, ROBERT L.
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; APPLICANT: GORRELL, JEFFREY R.
; APPLICANT: PHAM LAZARESCI, KATHLYN
; APPLICANT: LESTER, PHILIP M.
; APPLICANT: PENG, DAVID
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1939R1
; CURRENT APPLICATION NUMBER: US/10/356,974
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 60/354,579
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; US-10-356-974-2

Query Match      86.8%; Score 2181.5; DB 12; Length 449;
Best Local Similarity 90.6%; Pred. No. 2.4e-142;
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

Oy 20 EYQLLESGGGLVOPGGSLRLSCAASGFTFSNYAMSVMWRQAPGKGLEWVAISASGHSYLV 79
Db 1 EYQLVESGGGLVOPGGSLRLSCAASGFNIKDYIHHVRRQAPGKGLEWVAIRIPTYNGTYR 60
Oy 80 ADSVKGRTISRDNKNTLYLQNMNLSRAEDTAVYYCAKDR EYTMIVLVNG-----FDYW 134
Db 61 ADSVKGRTISRDNKNTLYLQNMNLSRAEDTAVYYCSR-----WGCGDFYAMDYV 110
Oy 133 GGGRTVTVSSASTKGPSVFPLAASSKSTSGGTRALGLCYKVFPEPVTVSMNSGALTSGV 194
Db 111 GGGTLVTVSSASTKGPSVFPLAASSKSTSGGTRALGLCYKVFPEPVTVSMNSGALTSGV 170
Oy 195 HTPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTRVDRVBPCKSCDKTHTCP 254
Db 171 HTPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTRVDRVBPCKSCDKTHTCP 230
Oy 255 PCPABELLGGPSVFLEPPPKPKDTLMIISRTPEVTCVVDVS HEDPEVKFMWYDGVENVNA 314
Db 231 PCPABELLGGPSVFLEPPPKPKDTLMIISRTPEVTCVVDVS HEDPEVKFMWYDGVENVNA 290
Oy 315 KTRPREQYNSTYRVYSVLTVLDHQMILNGEKYCKYSNKLAPAPIKTSKAKGQPREQ 374
Db 291 KTRPREQYNSTYRVYSVLTVLDHQMILNGEKYCKYSNKLAPAPIKTSKAKGQPREQ 350
Oy 375 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSGSEFFLY 434
Db 351 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSGSEFFLY 410
Oy 435 SKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPG 173
Db 411 SKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPG 149

RESULT 14
US-10-253-366-2
; Sequence 2, Application US/10253366
; Publication No. US20030078388A1
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1
; CURRENT APPLICATION NUMBER: US/10/253,366
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
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ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Sequence is synthesized.
 US-10-253-366-2

Query Match 86.8%; Score 2181.5; DB 15; Length 449;
 Best Local Similarity 90.6%; Pred. No. 2.4e-142;
 Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps -2;

QY 20 EVOLLESGGGLVOPGSLRLSCAASGFTFSNYAMSWVQAPGKLEWVSATISAGHSYTL 79
 Db 1 EVOLVESGGGLVOPGSLRLSCAASGFTFSNYAMSWVQAPGKLEWVSATISAGHSYTL 60
 QY 80 ADVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKREVTMIIVLNG-----FDYW 134
 Db 61 ADVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCSR-----WGDDGYAMDY 110
 QY 135 GQGTIRVYSSASTGSPVFLPAPSSKTSGGTALGCLVKDYFPEPTVSNVNSGALTSGV 194
 Db 111 GQGTIRVYSSASTGSPVFLPAPSSKTSGGTALGCLVKDYFPEPTVSNVNSGALTSGV 170
 QY 195 HTPFAVLQSSGLYSLSSVYTPSSSLGTQYICVNHKPSNTKYDKRVEPKSCDTHTCP 254
 Db 171 HTPFAVLQSSGLYSLSSVYTPSSSLGTQYICVNHKPSNTKYDKRVEPKSCDTHTCP 230
 QY 255 PCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGEVHNA 314
 Db 231 PCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGEVHNA 290
 QY 315 KTKPREQYNSTYRVSVLTGLVHODWLNKREYKCKVSKALPAPIEKTISKAKGQPREPQ 374
 Db 291 KTKPREQYNSTYRVSVLTGLVHODWLNKREYKCKVSKALPAPIEKTISKAKGQPREPQ 350
 QY 375 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLY 434
 Db 351 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLY 410
 QY 435 SKLTVDKSRMQQGNVFSCSVMEALHNHYTQKSLSLSPG 473
 Db 411 SKLTVDKSRMQQGNVFSCSVMEALHNHYTQKSLSLSPG 449

RESULT 15
 US-10-316-694-2
 Sequence 2, Application US/10316694
 Publication No. US20030118583A1
 GENERAL INFORMATION:
 APPLICANT: EMERY, JEFFERSON C.
 APPLICANT: MCDONALD, PAUL J.
 APPLICANT: O'LEARY, RHONA M.
 TITLE OF INVENTION: STABILIZING POLYPEPTIDES WHICH HAVE BEEN EXPOSED TO UREA
 FILE REFERENCE: P1940R1
 CURRENT APPLICATION NUMBER: US/10/316,694
 CURRENT FILING DATE: 2002-12-11
 PRIOR APPLICATION NUMBER: US 60/341,891
 PRIOR FILING DATE: 2001-12-19
 NUMBER OF SEQ ID NOS: 2
 SEQ ID NO 2
 LENGTH: 449
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Sequence is synthesized.
 US-10-316-694-2

Query Match 86.8%; Score 2181.5; DB 15; Length 449;
 Best Local Similarity 90.6%; Pred. No. 2.4e-142;
 Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

QY 20 EVOLLESGGGLVOPGSLRLSCAASGFTFSNYAMSWVQAPGKLEWVSATISAGHSYTL 79
 Db 1 EVOLVESGGGLVOPGSLRLSCAASGFTFSNYAMSWVQAPGKLEWVSATISAGHSYTL 60

QY 80 ADVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKREVTMIIVLNG-----FDYW 134
 Db 61 ADVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCSR-----WGDDGYAMDY 110
 QY 135 GQGTIRVYSSASTGSPVFLPAPSSKTSGGTALGCLVKDYFPEPTVSNVNSGALTSGV 194
 Db 111 GQGTIRVYSSASTGSPVFLPAPSSKTSGGTALGCLVKDYFPEPTVSNVNSGALTSGV 170
 QY 195 HTPFAVLQSSGLYSLSSVYTPSSSLGTQYICVNHKPSNTKYDKRVEPKSCDTHTCP 254
 Db 171 HTPFAVLQSSGLYSLSSVYTPSSSLGTQYICVNHKPSNTKYDKRVEPKSCDTHTCP 230
 QY 255 PCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGEVHNA 314
 Db 231 PCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGEVHNA 290
 QY 315 KTKPREQYNSTYRVSVLTGLVHODWLNKREYKCKVSKALPAPIEKTISKAKGQPREPQ 374
 Db 291 KTKPREQYNSTYRVSVLTGLVHODWLNKREYKCKVSKALPAPIEKTISKAKGQPREPQ 350
 QY 375 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLY 434
 Db 351 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLY 410
 QY 435 SKLTVDKSRMQQGNVFSCSVMEALHNHYTQKSLSLSPG 473
 Db 411 SKLTVDKSRMQQGNVFSCSVMEALHNHYTQKSLSLSPG 449

Search completed: September 12, 2003, 13:06:06
 Job time : 32.7966 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2003, 12:46:18 : Search time 39.9915 Seconds
(without alignments)
928.747 Million cell updates/sec

Title: US-09-848-832-4

Perfect score: 1223

Sequence: 1 MEAPAQQLFLLLMLPDTTG.....EVTHQGLSSPVTKSFNRGDC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_19Jun03:*

- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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- 18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	234	23	AAO14066
2	1223	100.0	234	24	ABU08018
3	1131	92.5	234	21	AA92239
4	1129	92.3	236	22	AA971272
5	1129	92.3	236	23	AB63490
6	1108.5	90.6	235	21	AA93702
7	1108.5	90.6	235	21	AA93729
8	1099.5	89.9	235	24	ABP71366
9	1096	89.6	234	21	AA93708

10	1096	89.6	234	21	AA93733	The kappa chain of Human anti-IgE Mab
11	1090	88.1	234	15	AA952951	The kappa chain of
12	1085.5	88.8	233	21	AA93704	The kappa chain of
13	1085.5	88.8	233	21	AA93731	The kappa chain of
14	1082.5	88.5	349	12	AA91218	IB1 IgG aberrant 1
15	1082.5	88.5	414	12	AA91311	IB1 IgG aberrant 1
16	1082.5	88.5	414	12	AA91308	IB1 IgG aberrant 1
17	1076	88.0	236	23	AA974299	Anti-human AILIM m
18	1066.5	87.2	238	24	AB941592	Human DITP antiIgE
19	1066	87.2	214	20	AA908599	Anti-human TNF- α lp
20	1066	87.2	236	23	AA974301	Anti-human AILIM m
21	1061	86.8	214	24	AB96296	4A5-3.1.1-B4 antiB
22	1061	86.8	224	22	AA975036	TRO005 HuMab kappa
23	1061	86.8	224	22	AA975037	TRO005 HuMab kappa
24	1057	86.4	224	22	AA999385	Human interleukin
25	1057	86.4	224	22	AA999388	Human interleukin
26	1057	86.4	224	22	AA999399	Human interleukin
27	1057	86.4	224	22	AA999372	Anti-IL8 monoclonal
28	1057	86.4	224	22	AA975031	Anti-IL8 monoclonal
29	1057	86.4	224	22	AA975032	Anti-IL8 monoclonal
30	1057	86.4	224	22	AA975034	TRO005 HuMab kappa
31	1056	86.3	234	22	AA936208	Human immune syste
32	1054	86.2	224	22	AA999371	Human interleukin
33	1054	86.2	224	22	AA975005	TRO005 HuMab kappa
34	1049	85.8	224	22	AA975039	TRO005 HuMab kappa
35	1046.5	85.6	234	24	AB95483	CJRA05 protein seq
36	1045	85.4	224	22	AA999386	Human interleukin
37	1045	85.4	224	22	AA975029	Anti-IL8 monoclonal
38	1043	85.3	224	22	AA999371	Human interleukin
39	1043	85.3	224	22	AA975004	Anti-IL8 monoclonal
40	1042	85.2	224	22	AA975038	TRO005 HuMab kappa
41	1028	84.1	224	22	AA975033	TRO005 HuMab kappa
42	1027	84.0	238	19	AA963034	Anti-Fas humanised
43	1027	84.0	238	21	AA914777	Humanised anti-Fas
44	1027	84.0	238	21	AA970927	Humanised HFE7A de
45	1027	84.0	238	23	AB974896	Humanised anti-Fas

ALIGNMENTS

RESULT 1	
AAO14066	
ID	AAO14066 standard; Protein: 234 AA.
XX	
AC	AAO14066:
XX	
DT	07-MAY-2002 (first entry)
XX	
DE	Light chain protein of the monoclonal antibody from clone JA.
XX	
XX	HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain;
KW	human monoclonal rabies virus neutralising antibody; immunoglobulin;
KW	light chain; central nervous system; CNS; prophylactic therapy; clone JA.
XX	
OS	Homo sapiens.
XX	
PN	WO200188132-A2.
XX	
PD	22-NOV-2001.
XX	
PF	04-MAY-2001; 2001WO-US14468.
XX	
PR	16-MAY-2000; 2000US-204518P.
XX	
XX	(UYJE-) UNIV JEFFERSON THOMAS.
PA	
XX	
PI	Hooper DC, Dietzschold B;
XX	
DR	WPI; 2002-062381/08.
XX	
XX	N-PSDB; AAK98702.
PT	Novel isolated human monoclonal rabies virus neutralising antibody


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FT Modified-site 72 /note= "potential protein kinase C phosphorylation site"
FT Modified-site 87 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 96 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 122 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 147..216 /note= "potential casein kinase II phosphorylation site"
FT Domain /label= immunoglobulin_domain
FT Domain 151..173 /label= signature_sequence
FT Modified-site 182 /note= "immunoglobulin"
FT Modified-site 184 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 190..233 /note= "potential casein kinase II phosphorylation site"
FT Domain /label= signature_sequence
FT Modified-site 202 /note= "immunoglobulin"
FT Domain /note= "potential casein kinase II phosphorylation site"
FT Domain 212..229 /label= signature_sequence
FT Domain /note= "immunoglobulin"
XX MO200020588-A2.
XX 13-APR-2000.
XX 01-OCT-1999; 99WO-US22908.
XX 02-OCT-1998; 98US-0165621.
XX (INCY-) INCYTE PHARM INC.
XX Tang YF, Corley NC, Guegler KJ, Lu DAM;
XX MPI: 2000-303775/26.
XX N-PSDB; AAA09154.
XX Purified polypeptide for treating or preventing disorders associated
XX with decreased expression or activity of bone marrow-derived serum
XX proteins
XX Claim 1; Page 68-69; 72pp; English.
XX Human bone marrow-derived serum proteins (BMDSP) 1 has chemical and
XX structural similarity with immunoglobulin kappa light chain. BMDSP-1
XX and BMDSP-2 are useful for treating or preventing a disorder associated
XX with decreased expression or activity of BMDSP.
XX Antagonists of BMDSP are useful for treating or preventing a disorder
XX associated with increased expression or activity of bone marrow-derived
XX serum proteins. The disorders include cancers (melanoma, adenocarcinoma,
XX sarcoma), immune disorders (acquired immunodeficiency syndrome (AIDS),
XX asthma, atherosclerosis, Crohn's disease, bronchitis, multiple sclerosis,
XX osteo- and rheumatoid arthritis), viral infections, parasitic infections,
XX schistosoma, tapeworm), and vascular disorders (arteriosclerosis,
XX hypertension, vasculitis).
XX Sequence 234 AA:
SQ
Query Match 92.5%; Score 1131; DB 21; Length 234;
Best Local Similarity 92.7%; Pred. No. 3,6e-64;
Matches 217; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
OY 1 MEAPQQLFLLMLPDTTGETIVLQSPATLSLSPGERATLACRASQTSRYLAWYQQR 60
DB 1 MEAPQQLFLLMLPDTTGETIVLQSPATLSLSPGERATLACRASQTSRYLAWYQQR 60
OY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLISLSEPEDPAVYVYCOQRNWPWFQ 120
DB 61 GOAPRLIYDASNRATGIPARFSGSGGTDFLISLSEPEDPAVYVYCOQYFTTPTFQ 120
```

```
OY 121 GTRKEFRNVAAVSVPFPSPDEQLKSGTASVYCLINFEYIPRAKVQKVDNALQSGNSQ 180
DB 121 GTRLEKRVVAAVSVPFPSPDEQLKSGTASVYCLINFEYIPRAKVQKVDNALQSGNSQ 180
OY 181 ESVTEGDSKDSYSLSTLTLSKADYKRVVACEVTHOGSSPVKSFNRCGC 234
DB 181 ESVTEGDSKDSYSLSTLTLSKADYKRVVACEVTHOGSSPVKSFNRCGC 234
RESULT 4
AAG71272
ID AAG71272 standard; Protein; 236 AA.
AC AAG71272;
XX 30-JUL-2001 (first entry)
XX Human gene 2-encoded secreted protein HTSER67, SEQ ID NO:121.
XX Human: secreted protein; proliferative disorder; cancer; chromosome 1;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX cardiovascular disorder; angiotensin disorder; kidney disorder;
XX gastrointestinal disorder; pregnancy-related disorder; tumour;
XX endocrine disorder; infection; wound healing; vulnery;
XX cell culture; chemotaxis; food additive;
XX binding partner identification.
XX Homo sapiens.
XX WO200132674-A1.
XX 10-MAY-2001.
XX 25-OCT-2000; 2000WO-US29360.
XX 29-OCT-1999; 99US-0162211.
XX 30-JUN-2000; 2000US-0215138.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Komatsoulis GA, Young PE, Moore PA;
XX MPI: 2001-291051/30.
XX N-PSDB; AAH31379.
XX New nucleic acid molecule encoding a human secreted protein, useful for
XX preventing, treating or ameliorating medical conditions such as
XX rheumatoid arthritis, Alzheimer's disease and microbial infections -
XX Claim 11; Page 498-499; 581pp; English.
XX AAH31349-AAH31428 represent cDNAs corresponding to 26 human secreted
XX protein genes, and AAG71243-AAG71319 represent the proteins they encode.
XX AAG71320-AAH31403 represent human secreted protein fragments. The genes
XX and their corresponding secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 52 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX proliferative disorders, cancer, tumours, foetal and developmental
XX abnormalities, haematopoietic disorders, diseases of the immune system,
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX allergies, neurological disorders (e.g., Alzheimer's disease,
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX cardiovascular disorders, angiogenic disorders, kidney disorders,
```

CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunoassort assay (ELISA). The present sequence represents a human
CC secreted protein of the invention.

SQ Sequence 236 AA;

Query Match 92.3%; Score 1129; DB 22; Length 236;

Best Local Similarity 92.4%; Pred. No. 4.8e-64;

Matches 218; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 1 MEAPQLFLLLMLPDTTGEIVLQSPATLSLSGEGATLACRASQTSRYLAWYQOKP 60
DB 1 MEXPAQLFLLLMLPDTTGEIVLQSPATLSLSGEGATLACRASQTSRYLAWYQOKP 60

QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLTLSLSLEPEDFAVYVCOQRFNMP--WTF 118
DB 61 GOAPRLIYXASXRATGIPARFSGSGGTDFLTLSLSLEPEDFAVYVCOQRFNMPXYTF 120

QY 119 GOGTVEFKRTVAASVFIPEPSDEQLKSGTASVCLLNFPYPREAKVQMKVDNALQSGN 178
DB 121 GXGTVKRTVAASVFIPEPSDEQLKSGTASVCLLNFPYPREAKVQMKVDNALQSGN 180

QY 179 SOESTVEDSKDSTYSLSTLTLSKADYEKKHVYACEVTHOGLSSPYKSFNRGEC 234
DB 181 SOESTVEDSKDSTYSLSTLTLSKADYEKKHVYACEVTHOGLSSPYKSFNRGEC 236

RESULT 5
ABG63490
ID ABG63490 standard; Protein: 236 AA.

XX ABG63490;

XX 27-AUG-2002 (first entry)

DE Human albumin fusion protein #165.

KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytoskeletal; antinfectility; antiinflammatory; antitumor;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; antiarthritic.

XX Homo sapiens.
OS Synthetic.

XX WO200177137-A1.

XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-US11988.

XX 12-APR-2000; 2000US-229358P.

XX 25-APR-2000; 2000US-199384P.

XX 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Haseltine WA;

XX WPI: 2002-010886/01.

XX New fusion protein for treating disease e.g. diabetes comprises an
PT albumin fused to a therapeutic protein -
PS Claim 1; Page 682; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein X and human albumin (HA, also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or
CC disorder that may be modulated by therapeutic protein X. The albumin
CC extends the shelf-life of protein X, and may increase its biological
CC in vitro/in vivo activity. The protein is useful for treating and
CC diagnosing disorders such as cancer, reproductive disorders, digestive
CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
CC (e.g. diabetes), haematopoietic disorders, neural disorders
CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
CC fusion proteins of the invention.

SQ Sequence 236 AA;

Query Match 92.3%; Score 1129; DB 23; Length 236;

Best Local Similarity 92.4%; Pred. No. 4.8e-64;

Matches 218; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 1 MEAPQLFLLLMLPDTTGEIVLQSPATLSLSGEGATLACRASQTSRYLAWYQOKP 60
DB 1 MEXPAQLFLLLMLPDTTGEIVLQSPATLSLSGEGATLACRASQTSRYLAWYQOKP 60

QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLTLSLSLEPEDFAVYVCOQRFNMP--WTF 118
DB 61 GOAPRLIYXASXRATGIPARFSGSGGTDFLTLSLSLEPEDFAVYVCOQRFNMPXYTF 120

QY 119 GOGTVEFKRTVAASVFIPEPSDEQLKSGTASVCLLNFPYPREAKVQMKVDNALQSGN 178
DB 121 GXGTVKRTVAASVFIPEPSDEQLKSGTASVCLLNFPYPREAKVQMKVDNALQSGN 180

QY 179 SOESTVEDSKDSTYSLSTLTLSKADYEKKHVYACEVTHOGLSSPYKSFNRGEC 234
DB 181 SOESTVEDSKDSTYSLSTLTLSKADYEKKHVYACEVTHOGLSSPYKSFNRGEC 236

RESULT 6
AAV93702
ID AAV93702 standard; Protein: 235 AA.

XX AAV93702;

XX 03-OCT-2000 (first entry)

DE The kappa chain of immunoglobulin clone 4.1.1.

KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.

XX Homo sapiens.

XX WO200037504-A2.

XX 29-JUN-2000.

XX 23-DEC-1999; 99WO-US30895.

XX 23-DEC-1998; 98US-0113647.

XX (PFIZ) PFIZER INC.

XX (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

XX Corvalan JR;

XX MPI: 2000-442647/38.
 DR N-PSDB: AAA46865.
 XX
 PR Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 XX
 PS Claim 3; Fig 1A; 157pp; English.
 XX
 XX The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FR1-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 CC
 XX Sequence 235 AA:
 SQ
 Query Match 90.6%; Score 1108.5; DB 21; Length 235;
 Best Local Similarity 91.5%; Pred. No. 9.5e-63;
 Matches 215; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
 QY 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQK 59
 DB 1 METPAQLFLLLMLPDTTGEIVLTQSPGTLISLSPGERATLSCRASQSISSFLAWYQQR 60
 QY 60 PGQAPRLIYDTSNRATGIPARFSGSGGTPTLTSSLEPEDPAVYVCCQGFNMPFTFG 119
 DB 61 PGQAPRLIYDTSNRATGIPARFSGSGGTPTLTSSLEPEDPAVYVCCQGFNMPFTFG 120
 QY 120 QGTKEFERFRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVOMKVDNALQSGNS 179
 DB 121 QGTKEFERFRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVOMKVDNALQSGNS 180
 QY 180 QESVTEODSKDSTVSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234
 DB 181 QESVTEODSKDSTVSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 235

RESULT 7
 AAY93729
 ID AAY93729 standard; Protein: 235 AA.
 XX
 AC AAY93729;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE The kappa chain of immunoglobulin clone 4.1.1.
 XX
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"
 XX
 PN WO200037504-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 23-DEC-1999; 99WO-US30895.
 XX
 PR 23-DEC-1998; 98US-0113647.
 XX

PA (Pfiz.) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 DR MPI: 2000-442647/38.
 DR N-PSDB: AAA46893.
 XX
 XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 XX
 PS Claim 3; Fig 22g; 157pp; English.
 XX
 XX The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FR1-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 CC
 XX Sequence 235 AA:
 SQ
 Query Match 90.6%; Score 1108.5; DB 21; Length 235;
 Best Local Similarity 91.5%; Pred. No. 9.5e-63;
 Matches 215; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
 QY 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQK 59
 DB 1 METPAQLFLLLMLPDTTGEIVLTQSPGTLISLSPGERATLSCRASQSISSFLAWYQQR 60
 QY 60 PGQAPRLIYDTSNRATGIPARFSGSGGTPTLTSSLEPEDPAVYVCCQGFNMPFTFG 119
 DB 61 PGQAPRLIYDTSNRATGIPARFSGSGGTPTLTSSLEPEDPAVYVCCQGFNMPFTFG 120
 QY 120 QGTKEFERFRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVOMKVDNALQSGNS 179
 DB 121 QGTKEFERFRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVOMKVDNALQSGNS 180
 QY 180 QESVTEODSKDSTVSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234
 DB 181 QESVTEODSKDSTVSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 235

RESULT 8
 ABP71366
 ID ABP71366 standard; Protein: 235 AA.
 XX
 AC ABP71366;
 XX
 DT 28-APR-2003 (first entry)
 XX
 DE Anti-OPGL-1 antibody kappa light chain.
 XX
 KW Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;
 KW antichrithic; cytoslatic; OPGL; anti-OPGL-1; antibody.
 XX
 OS Mus musculus.
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Igc2 signal peptide"
 FT Region 21..128
 FT /note= "variable region"
 FT Region 129..235
 FT /note= "constant region"
 XX

PN WO2003002713-A2.
XX
XX 09-JAN-2003.
XX
XX 25-JUN-2002; 2002WO-US20181.
XX
XX 26-JUN-2001; 2001US-301172P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX (ABGE-) AMGEN INC.
XX
XX Boyle WJ, Martin RH, Corvalan JR, Davis GC;
XX
XX WPI: 2003-210262/20.
XX
XX N-PSDB: AB259148.
XX
XX
XX New antibodies that interact with osteoprotegerin ligands, useful for
XX
XX treating osteoporosis disorders, e.g. osteoporosis, bone loss from
XX
XX arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia
XX
XX and osteonecrosis.
XX
XX
XX Claim 1; Fig 4; 144pp; English.
XX
XX The invention relates to antibodies that interact with osteoprotegerin
XX
XX ligands (OPGL). The antibody is useful for detecting the level of OPGL in
XX
XX a biological sample. The antibody, or the pharmaceutical composition
XX
XX comprising the antibody, is also useful for treating osteoporosis disorder,
XX
XX an inflammatory condition with attendant bone loss, an autoimmune
XX
XX condition with attendant bone loss in a patient or rheumatoid arthritis
XX
XX in a patient. In particular, the antibody or composition is useful for
XX
XX treating bone diseases, e.g. osteoporosis, bone loss from arthritis,
XX
XX Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
XX
XX syndrome or acromegaly), osteogenesis imperfecta, homocystinuria,
XX
XX Marfan's syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or
XX
XX osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
XX
XX kappa light chain.
XX
XX
XX Sequence 235 AA:
SQ
Query Match 89.9%; Score 1099.5; DB 24; Length 235;
Best Local Similarity 91.5%; Pred. No. 3.5e-62;
Matches 215; Conservative 6; Mismatches 13; Indels 1; Gaps 1;
QY 1 MEAPQALLFLLLMLPPTTGEIVLTOSPATLSLSPGERATLACRASQTA-SRYLAWYQOK 59
DB 1 MEAPQALLFLLLMLPPTTGEIVLTOSPATLSLSPGERATLACRASQTA-SRYLAWYQOK 60
QY 60 PGQAPRLIYDTSNRATGIPARFSGSGGTDFTLTISSLKPEDFATVYCCQGRFNPMTFG 119
DB 61 PGQAPRLIYDTSNRATGIPARFSGSGGTDFTLTISSLKPEDFATVYCCQGRFNPMTFG 120
QY 120 QGTVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYRPAKQVMKDNALQSGNS 179
DB 121 QGTVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYRPAKQVMKDNALQSGNS 180
QY 180 QESTVEDSKDSTYLSSTLTLSKADYEKKHKKYACEVTHQGLSSPVTKSFNRGEC 234
DB 181 QESTVEDSKDSTYLSSTLTLSKADYEKKHKKYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 9
AAV93708
ID AAV93708 standard; Protein: 234 AA.
XX
XX AAV93708;
XX
XX
XX 03-OCT-2000 (first entry)
XX
XX The kappa chain of immunoglobulin clone 6.1.1.
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX
XX hyperimmune disorder; autoimmune disease; diabetes; graft rejection;
XX
XX proliferative disorder; cancer; immunodeficient disorder.

XX
XX Homo sapiens.
OS
XX
XX WO200037504-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US30895.
XX
XX 23-DEC-1998; 98US-0113647.
XX
XX
XX (PRIZ) PRIZER INC.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX
XX Corvalan JR;
XX
XX WPI: 2000-442647/38.
XX
XX N-PSDB: AAA46871.
XX
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
XX
XX (CTLA)-4 containing specified heavy and light chain sequences, useful
XX
XX for treating, e.g. immune disorders.
XX
XX
XX Claim 3; Fig 1D; 157pp; English.
XX
XX The present sequence represents a kappa chain of an antibody of the
XX
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen
XX
XX (CTLA)-4. Antibodies of the invention are composed of a heavy chain
XX
XX variable region, comprising a modified contiguous sequence from a
XX
XX FRI-FR3 sequence encoded by a human VH3-33 family gene. The
XX
XX modifications are contained in CDRI, CDR2 and/or framework regions.
XX
XX The antibodies may be used to inhibit CTLA-4 and down-regulate the
XX
XX immune system to treat hyperimmune disorders (e.g. autoimmune
XX
XX disease, diabetes and graft rejection) and proliferative disorders
XX
XX (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
XX
XX immune system to up-regulate immunodeficient disorders.
XX
XX
XX Sequence 234 AA:
SQ
Query Match 89.6%; Score 1096; DB 21; Length 234;
Best Local Similarity 91.0%; Pred. No. 5.8e-62;
Matches 213; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
QY 1 MEAPQALLFLLLMLPPTTGEIVLTOSPATLSLSPGERATLACRASQTA-SRYLAWYQOK 60
DB 1 MEAPQALLFLLLMLPPTTGEIVLTOSPATLSLSPGERATLACRASQTA-SRYLAWYQOK 60
QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFTLTISSLKPEDFATVYCCQGRFNPMTFG 120
DB 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFTLTISSLKPEDFATVYCCQGRFNPMTFG 120
QY 121 GTRVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYRPAKQVMKDNALQSGNS 180
DB 121 GTRVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYRPAKQVMKDNALQSGNS 180
QY 181 ESYTEQDSKSTYLSSTLTLSKADYEKKHKKYACEVTHQGLSSPVTKSFNRGEC 234
DB 181 ESYTEQDSKSTYLSSTLTLSKADYEKKHKKYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 10
AAV93733
ID AAV93733 standard; Protein: 234 AA.
XX
XX AAV93733;
XX
XX
XX 03-OCT-2000 (first entry)
XX
XX The kappa chain of immunoglobulin clone 6.1.1.
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX
XX hyperimmune disorder; autoimmune disease; diabetes; graft rejection;
XX
XX proliferative disorder; cancer; immunodeficient disorder.

```

KW proliferative disorder; cancer; immunodeficient disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "signal peptide"
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US30895.
XX
PR 23-DEC-1998; 98US-0113647.
XX
PA (PF12 ) PEIZER INC.
XX (ABGE-) ABGENIX INC.
XX
PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG,
PI Corvalan JR;
XX
DR WPI: 2000-442647/38.
DR N-PSDB; AAA46897.
XX
XX
PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT (CTLA)-4 containing, specified heavy and light chain sequences, useful
PT for treating, e.g. immune disorders.
XX
PS Claim 3; Fig 22o; 157pp; English.
XX
CC The present sequence represents a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDRI, CDRI2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.
XX
SQ Sequence 234 AA:
Query Match 89.6%; Score 1096; DB 21; Length 234;
Best Local Similarity 91.0%; Pred. No. 5,8e-62;
Matches 213; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
QY 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATISLSPGERATLACRASQTSRLIAYQOKP 60
DB 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATISLSPGERATLACRASQTSRLIAYQOKP 60
QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLTLSLEPEDFAVYYCOQRNMPWTFQ 120
DB 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLTLSLEPEDFAVYYCOQRNMPWTFQ 120
QY 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVDNALQSGNSQ 180
DB 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVDNALQSGNSQ 180
QY 181 ESYTQDSKDSYISLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSPNRGEC 234
DB 181 ESYTQDSKDSYISLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSPNRGEC 234

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DT 27-OCT-1994 (first entry)
XX
DE Human anti-IgE MAb light chain.
XX
KW Human IgE; CH4 region; triggers mediator release;
KW Mast cells; Monoclonal antibody; allergy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 21..128
FT /label= light chain variable region
XX
PN EP592230-A1.
XX
PD 13-APR-1994.
XX
PF 07-OCT-1993; 93EP-0308006.
XX
PR 07-OCT-1992; 92JP-0293800.
XX
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;
PI Yoshida T;
XX
DR WPI: 1994-120330/15.
DR N-PSDB; AAQ71872.
XX
XX
PT Human monoclonal anti-IgE peptide antibody - inhibits histamine
PT release from mast cells by allergen stimulation, useful for
PT preventing allergies
XX
PS Claim 3; Page 12; 21pp; English.
XX
CC AAR52951 shows the light chain of a human type anti-IgE peptide
CC monoclonal antibody which inhibits the signal transmission for
CC the release of chemical mediator from mast cells and basophils
CC stimulated with allergen. The antibody can be used for the
CC prophylaxis and the therapy of allergy.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 234 AA:
Query Match 89.1%; Score 1090; DB 15; Length 234;
Best Local Similarity 89.3%; Pred. No. 1,4e-61;
Matches 209; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATISLSPGERATLACRASQTSRLIAYQOKP 60
DB 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATISLSPGERATLACRASQTSRLIAYQOKP 60
QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLTLSLEPEDFAVYYCOQRNMPWTFQ 120
DB 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLTLSLEPEDFAVYYCOQRNMPWTFQ 120
QY 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVDNALQSGNSQ 180
DB 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVDNALQSGNSQ 180
QY 181 ESYTQDSKDSYISLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSPNRGEC 234
DB 181 ESYTQDSKDSYISLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSPNRGEC 234

```

RESULT 11

```

AAR52951
ID AAR52951 standard; Protein; 234 AA.
XX
AC AAR52951;
XX
DT 25-MAR-2003 (updated)

```

RESULT 12

```

AAR53704
ID AAR53704 standard; Protein; 233 AA.
XX
AC AAR53704;
XX
DT 03-OCT-2000 (first entry)
XX

```

DE The kappa chain of immunoglobulin clone 4.8.1.
 XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200037504-A2.
 XX
 PD 29-JUN-2000.
 XX
 XX 23-DEC-1999; 99WO-US30895.
 XX
 PR 23-DEC-1998; 98US-0113647.
 XX
 PA (Pfizer) Pfizer Inc.
 XX (ABGE-) ABGENIX INC.
 XX
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 DR MPI: 2000-442647/38.
 DR N-PSDB: AAA46867.
 XX
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 XX
 PS Claim 3; Fig 1B; 157pp; English.
 XX
 CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 CC
 XX
 SQ Sequence 233 AA:
 Query Match 88.8%; Score 1085.5; DB 21; Length 233;
 Best Local Similarity 91.0%; Pred. No. 2.7e-61;
 Matches 213; Conservative 5; Mismatches 15; Indels 1; Gaps 1;
 Oy 1 MEAPQLFLLLMLPPTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQKP 60
 Db 1 METPAQLFLLLMLPDTTGEIVLTQSPGTLISLSPGERATLSCRTS-VSSSYLAWYQKP 59
 Oy 61 GOAPRLLYDTSNRATGIPARFSGSGSTDTFTLSSLEPPDFAVYYCQGRFNNPWTGQ 120
 Db 60 GOAPRLLYGASNRATGIPDRFSGSGSTDTFTLTSLRLEPDPFAYYYCQYGISPFTGG 119
 Oy 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVNALQSGNSQ 180
 Db 120 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVNALQSGNSQ 179
 Oy 181 ESVTEQDSKSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTYSFNNGEC 234
 Db 180 ESVTEQDSKSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTYSFNNGEC 233

RESULT 13

AA93731

ID AA93731 standard; Protein; 233 AA.

DT 03-OCT-2000 (first entry)

XX
 DE The kappa chain of immunoglobulin clone 4.8.1.
 XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200037504-A2.
 XX
 PD 29-JUN-2000.
 XX
 XX 23-DEC-1999; 99WO-US30895.
 XX
 PR 23-DEC-1998; 98US-0113647.
 XX
 PA (Pfizer) Pfizer Inc.
 XX (ABGE-) ABGENIX INC.
 XX
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 DR MPI: 2000-442647/38.
 DR N-PSDB: AAA46895.
 XX
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 XX
 PS Claim 3; Fig 22k; 157pp; English.
 XX
 CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 CC
 XX
 SQ Sequence 233 AA:
 Query Match 88.8%; Score 1085.5; DB 21; Length 233;
 Best Local Similarity 91.0%; Pred. No. 2.7e-61;
 Matches 213; Conservative 5; Mismatches 15; Indels 1; Gaps 1;
 Oy 1 MEAPQLFLLLMLPPTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQKP 60
 Db 1 METPAQLFLLLMLPDTTGEIVLTQSPGTLISLSPGERATLSCRTS-VSSSYLAWYQKP 59
 Oy 61 GOAPRLLYDTSNRATGIPARFSGSGSTDTFTLSSLEPPDFAVYYCQGRFNNPWTGQ 120
 Db 60 GOAPRLLYGASNRATGIPDRFSGSGSTDTFTLTSLRLEPDPFAYYYCQYGISPFTGG 119
 Oy 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVNALQSGNSQ 180
 Db 120 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVNALQSGNSQ 179
 Oy 181 ESVTEQDSKSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTYSFNNGEC 234
 Db 180 ESVTEQDSKSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTYSFNNGEC 233

RESULT 14

AAR12128

ID	AA	12128	standard; Protein: 349 AA.
XX	AA	12128:	
AC	AA	12128:	
XX	25-MAR-2003	(updated)	
DT	01-AUG-1991	(first entry)	
DE	1B1 IgG aberrant light chain with duplicated variable region.		
XX			
KW	immunoglobulin G; light chain; variable region; duplication;		
KM	passive immunity; group B streptococci.		
XX			
OS	Homo sapiens.		
XX			
FX	Key	Location/Qualifiers	
FT	Peptide	1..17	
FT	Region	/label= leader peptide	
FT	Region	18..130	
FT	Region	/label= variable region	
FT	Region	/note= "L/V 1"	
FT	Region	131..243	
FT	Region	/label= variable region	
FT	Region	/note= "L/V 2"	
FT	Region	244..345	
FT	Region	/label= constant region	
XX			
PN	W09106305-A.		
XX			
PD	16-MAY-1991.		
XX			
PF	06-NOV-1990;	90WO-US06426.	
XX			
PR	07-NOV-1989;	89US-0432700.	
XX			
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.		
XX			
PI	Shuford WM, Harris LJ, Rafi HV;		
XX			
DR	WPI: 1991-163947/22.		
DR	N-PSDB; AAQ11878.		
XX			
PT	Oligomeric immunoglobulin(s) with high avidity for antigen(s) -		
PT	formed by duplicating esp. variable region of light chain of IgG		
PT	class		
XX			
PS	Example 5; Fig 16; 104pp; English.		
XX			
CC	This sequence is deduced from the cDNA clone 4B9-VK15 and includes		
CC	the amino acid sequence beyond the first stop codon. The clone is		
CC	incomplete, starting from the G of the ATG initiator codon, but the		
CC	initial Met is given. Antibody molecules of the invention can		
CC	include one or two aberrant light chains containing a duplicated		
CC	variable region, to produce heavier antibodies. These heavier		
CC	antibodies were found to have higher avidity than antibodies with		
CC	just a single copy of the L/V region. The antibodies can be used to		
CC	treat disease, e.g. infection by Streptococcus agalactiae. They are		
CC	able to pass across the placenta.		
CC	See also AAQ11879 and AAQ11880.		
CC	(Updated on 25-MAR-2003 to correct PA field.)		
XX			
XX	Sequence	349 AA;	
XX			
XX	Query Match	88.5%; Score 1082.5; DB 12; Length 349;	
XX	Best Local Similarity	63.6%; Pred. No. 6e-61;	
XX	Matches 222; Conservative	3; Mismatches 9; Indels 115; Gaps 2	
QY	1	MEADPAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQOKP	60
DB	1	MEADPAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQVGSYLAAYQOKP	60
DB	61	GOARRLILYDTSNRATGIPARFSGSGSTDTLTLSISLEPEDFAVYYCOQRFNWP-----	115
DB	61	GOARRLILYDTSNRATGIPARFSGSGSTDTLTLTSSLEPEDFAVYYCOHRDNMPGATF	120

Qy	116	-----	115
Db	121	GGGTKEIKHTGEIVLTQSPATLSLSPGERATLSCRASQIVGSYLAWYQOKPGQAPRL	180
Qy	116	-----	125
Db	181	ITYDASNATGCIPIARFSGSGGSTDFTLTITSLPEEDFAVYYIQHRDNNPFGATFEGGTRKVE	240
Qy	126	FKRTVAAPSVFIFPPSDSOLKSGTASVYCLINNEYPREAKYQMKVDNALQSGNSQESVTE	185
Db	241	IKRTVAAPSVFIFPPSDSOLKSGTASVYCLINNEYPREAKYQMKVDNALQSGNSQESVTE	300
Qy	186	QDSKDSYVSLSSITLTLKADYEKKRYVACEPTHGGLSSPVFKSTNRREC	234
Db	301	QDSKDSYVSLSSITLTLKADYEKKRYVACEPTHGGLSSPVFKSTNRREC	349
RESULT 15			
ID	AA13111	standard; Protein: 414 AA.	
XX	AA13111;		
AC			
XX	25-MAR-2003 (updated)		
DT	01-AUG-1991 (first entry)		
XX			
DE	1B1 IgG aberrant light chain with duplicated variable region.		
XX			
KW	immunoglobulin G; light chain; variable region; duplication;		
KW	passive immunity; group B streptococci.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..17	
FT	Region	/label= leader peptide	
FT	Region	18..130	
FT	Region	/label= variable region	
FT	Region	/note= "L/V 1"	
FT	Region	131..243	
FT	Region	/label= variable region	
FT	Region	/note= "L/V 2"	
FT	Region	244..345	
FT	Region	/label= constant region	
XX			
PN	WO9106305-A.		
XX			
PD	16-MAY-1991.		
XX			
PF	06-NOV-1990;	90WO-US06426.	
XX			
PR	07-NOV-1989;	89US-0432700.	
XX			
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.		
PI	Shuford WM, Harris LJ, Raff HV;		
XX			
DR	WPI; 1991-163947/22.		
DR	N-PSDB; AAQ11878.		
XX			
PT	Oligomeric immunoglobulin(s) with high avidity for antigen(s) -		
PT	formed by duplicating esp. variable region of light chain of IgG		
PT	class		
XX			
PS	Example 5; Fig 16; 104pp; English.		
XX			
CC	This sequence is deduced from the cDNA clone 4B9-VK15 and includes		
CC	the amino acid sequence beyond the first stop codon ("x" in the		
CC	sequence represents a nonsense codon). The clone is incomplete,		
CC	starting from the G of the ATG initiator codon, but the initial Met		
CC	is given. Antibody molecules of the invention can include one or two		
CC	aberrant light chains containing a duplicated variable region, to		

CC produce heavier antibodies. These heavier antibodies were found to
 CC have higher avidity than antibodies with just a single copy of the
 CC L/V region. The antibodies can be used to treat disease, e.g.
 CC infection by streptococcus agalactiae. They are able to pass across
 CC the placenta.
 CC See also AAQ11879 and AAQ11880.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX

SQ Sequence 414 AA:

Query Match 88.5%: Score 1082.5: DB 12: Length 414;
 Best Local Similarity 63.6%: Pred. No. 7.1e-61;
 Matches 222: Conservative 3: Mismatches 9: Indels 115: Gaps 2;

```

QY 1 MEAPQLLELLMLPDTGGEIVLTQSPATLSLSPGERATLACRASQTSRYLAMYQOKP 60
   |||||
Db 1 MEAPQLLELLMLPDTGGEIVLTQSPATLSLSPGERATLACRASQTSRYLAMYQOKP 60
   |||||

QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFTLTISSLEPEDFAVYCCQARPMP----- 115
   |||||
Db 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFTLTISSLEPEDFAVYCCQHRDNPFGATF 120
   |||||

QY 116 ----- 115
Db 121 GGGTVEIKHTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAMYQOKPQAPRPL 180
   |||||

QY 116 -----TFGGTKVE 125
Db 181 IYDASNRATGIPARFSGSGGTDFTLTISSLEPEDFAVYCCQHRDNPFGATFGGTKVE 240
   |||||

QY 126 EKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKYQWKVDNALQSGNSQESVTE 185
   |||||
Db 241 IKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKYQWKVDNALQSGNSQESVTE 300
   |||||

QY 186 QDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234
   |||||
Db 301 QDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 349
   |||||

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Search completed: September 12, 2003, 13:00:41
 Job time : 41.9915 secs

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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:58:39 ; Search time 26.7797 Seconds

(without alignments)
748.902 Million cell updates/sec

Title: US-09-848-832-3

Perfect score: 2514

Sequence: 1 MEFLSWFLVAILKGVQCE.....MHEALHNHYTKSLSPGK 474

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2221.5	88.4	459	1	US-08-157-101A-7 Sequence 7, Appl
2	2193.5	87.3	452	3	US-09-027-449-71 Sequence 71, Appl
3	2193.5	87.3	452	3	US-09-026-985-71 Sequence 71, Appl
4	2193.5	87.3	452	4	US-09-121-952A-71 Sequence 71, Appl
5	2193.5	87.3	452	4	US-09-234-340A-71 Sequence 8, Appl
6	2183	86.8	478	3	US-08-487-550-8 Sequence 71, Appl
7	2183	86.8	478	4	US-09-526-098-8 Sequence 8, Appl
8	2181.5	86.8	449	4	US-09-679-397-2 Sequence 2, Appl
9	2181.5	86.8	449	4	US-09-680-148-2 Sequence 2, Appl
10	2181.5	86.8	449	4	US-09-304-465A-2 Sequence 2, Appl
11	2178	86.6	453	3	US-08-466-151-8 Sequence 8, Appl
12	2178	86.6	453	4	US-08-466-151-8 Sequence 8, Appl
13	2173	86.4	451	2	US-08-887-352B-18 Sequence 18, Appl
14	2173	86.4	451	3	US-09-109-207C-18 Sequence 18, Appl
15	2173	86.4	451	3	US-09-282-505-2 Sequence 2, Appl
16	2173	86.4	451	3	US-09-054-255-2 Sequence 2, Appl
17	2173	86.4	451	3	US-09-296-005-18 Sequence 18, Appl
18	2173	86.4	451	4	US-09-282-846-2 Sequence 2, Appl
19	2173	86.4	451	4	US-09-680-145-2 Sequence 2, Appl
20	2170	86.3	451	2	US-08-887-352B-14 Sequence 14, Appl
21	2170	86.3	451	3	US-08-887-352B-16 Sequence 16, Appl
22	2170	86.3	451	3	US-08-466-151-65 Sequence 65, Appl
23	2170	86.3	451	3	US-09-109-207C-14 Sequence 14, Appl
24	2170	86.3	451	3	US-09-109-207C-16 Sequence 16, Appl
25	2170	86.3	451	3	US-09-296-005-14 Sequence 16, Appl
26	2170	86.3	451	3	US-09-296-005-16 Sequence 16, Appl
27	2117	84.2	476	2	US-08-378-939-10 Sequence 10, Appl

28	2113	84.0	443	5	PCT-US96-13152-4 Sequence 4, Appl
29	2104.5	83.7	467	1	US-08-704-744-81 Sequence 81, Appl
30	2100.5	83.6	468	4	US-09-485-737B-67 Sequence 67, Appl
31	2100.5	83.6	711	4	US-09-485-737B-90 Sequence 90, Appl
32	2094.5	83.3	467	3	US-09-049-672A-8 Sequence 8, Appl
33	2092	83.2	476	3	US-08-487-550-12 Sequence 12, Appl
34	2092	83.2	476	4	US-09-526-098-12 Sequence 12, Appl
35	2090.5	83.2	473	3	US-09-049-672A-4 Sequence 4, Appl
36	2089	83.1	449	1	US-08-458-516-13 Sequence 13, Appl
37	2086.5	83.0	446	3	US-08-397-411-7 Sequence 7, Appl
38	2062	82.0	472	4	US-08-793-450-8 Sequence 8, Appl
39	2062	82.0	472	4	US-09-301-593-43 Sequence 43, Appl
40	2060	81.9	472	4	US-09-301-593-30 Sequence 30, Appl
41	2046	81.4	476	4	US-08-487-550-4 Sequence 4, Appl
42	2046	81.4	476	4	US-09-526-098-4 Sequence 4, Appl
43	2044.5	81.3	453	4	US-09-301-593-18 Sequence 18, Appl
44	2037	81.0	451	4	US-09-247-352-3 Sequence 3, Appl
45	2037	81.0	451	4	US-09-466-635-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-157-101A-7
Query Match 88.4%; Score 2221.5; DB 1; Length 459;
Best Local Similarity 89.9%; Pred. No. 2,1e-172;
Matches 417; Conservative 19; Mismatches 23; Indels 5; Gaps 1;

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QY 11 VALIKGYOCEVLELSEGGGLVOPGSLRLSCAASGFTFSNYSAMVROAPGKLEWVSAT 70
D 1 VGLLRGVOQVQLVESGGGVQPGRLSLRSCAASGFTFSNYSAMVROAPGKLEWVAVI 60
QY 71 SASGHSYVLADSVKGRFTISRDNSKNTLYIQMNSLRADDAVYYCAKDREVTMTIVLNGG 130
D 61 LYDENHNFYADSVKGRFTISRDNKNTLYIEVKSLQEDTGVYCIIRDQTYGV-----HR 115
QY 131 FDYVGGTFRVYVSSASTKGPVFLAPLPSKSTSGCTALGCLVMDYFPEPTVSMNSGAL 190
D 116 FDSGGGLTVYVSSASTKGPVFLAPLPSKSTSGCTALGCLVMDYFPEPTVSMNSGAL 175
QY 191 TSVGHTPEPALQSSGLYSLSVTVTPSSSLGTQTYICVNHKPSNTKYDKKVEPKSCDKT 250
D 176 ASGVHTPEPALQSSGLYSLSVTVTPSSSLGTQTYICVNHKPSNTKYDKKVEPKSCDKT 235
QY 251 HTCPPCAPAPLGGPSVFLPPPKPKDTLMSRTEPVTCVVVDVSHEDPEVKFNNYVDSGE 310
D 236 HTCPPCAPAPLGGPSVFLPPPKPKDTLMSRTEPVTCVVVDVSHEDPEVKFNNYVDSGE 295
QY 311 VHNKTKPREQYNSTYRVYVSLTVLHODMNLNGKEYCKVSNKALPAPIETISKAKGQP 370
D 296 VHNKTKPREQYNSTYRVYVSLTVLHODMNLNGKEYCKVSNKALPAPIETISKAKGQP 355
QY 371 REPOVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPVLDSDGS 430
D 356 REPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPVLDSDGS 415
QY 431 FFYLSKLTVDKSRMQGNVFCSVNHEALNHNHYTKSLSPGK 474
D 416 FFYLSKLTVDKSRMQGNVFCSVNHEALNHNHYTKSLSPGK 459
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RESULT 2

```
US-09-027-449-71
: Sequence 71, Application US/09027449
: Patent No. 6025158
: GENERAL INFORMATION:
: APPLICANT: Gonzalez, Tania R.
: APPLICANT: Leong, Steven R.
: APPLICANT: Presta, Leonard G.
: TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
: TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatlin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/027,449
: FILING DATE: 20-Feb-1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/074,330
: FILING DATE: 22-Jan-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/038,664
: FILING DATE: 21-Feb-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P1085R3-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/952-9881
```

```
: INFORMATION FOR SEQ ID NO: 71:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 452 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-09-027-449-71
```

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Query Match 87.3%; Score 2193.5; DB 3; Length 452;
Best Local Similarity 91.2%; Pred. No. 3.8e-170; Indels 7; Gaps 2;
Matches 417; Conservative 9; Mismatches 24;
```

```
QY 20 EVQLLEGGGGLVQGGSLRLSCAASGFTFSNYSAMVROAPGKLEWVSATISASGHSYTL 79
D 1 EVQLVQGGGGLVQGGSLRLSCAASGFTFSNYSAMVROAPGKLEWVGIDPSNGEFTY 60
QY 80 ADSVKGRTISRDNKNTLYIQMNSLRADDAVYYCAKDREVTMTIVLNGG- FDYVGG 137
D 61 NQKFGRTLSRDNSKNTAYLQMNSLRADDAVYYCARGD-----YRYNGDMFEDVWGG 115
QY 138 TRVTYVSSASTKGPVFLAPLPSKSTSGCTALGCLVMDYFPEPTVSMNSGALTSVHTF 197
D 116 TLVTYVSSASTKGPVFLAPLPSKSTSGCTALGCLVMDYFPEPTVSMNSGALTSVHTF 175
QY 198 PAVLQSSGLYSLSVTVTPSSSLGTQTYICVNHKPSNTKYDKKVEPKSCDKTHTCPCP 257
D 176 PAVLQSSGLYSLSVTVTPSSSLGTQTYICVNHKPSNTKYDKKVEPKSCDKTHTCPCP 235
QY 258 APELLGGPSVFLPPPKPKDTLMSRTEPVTCVVVDVSHEDPEVKFNNYVDSGEVHNKTK 317
D 236 APELLGGPSVFLPPPKPKDTLMSRTEPVTCVVVDVSHEDPEVKFNNYVDSGEVHNKTK 295
QY 318 PREQYNSTYRVYVSLTVLHODMNLNGKEYCKVSNKALPAPIETISKAKGPREPOVYT 377
D 296 PREQYNSTYRVYVSLTVLHODMNLNGKEYCKVSNKALPAPIETISKAKGPREPOVYT 355
QY 378 LPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPVLDSDGSFFLYSKL 437
D 356 LPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPVLDSDGSFFLYSKL 415
QY 438 TVDKSRMQGNVFCSVNHEALNHNHYTKSLSPGK 474
D 416 TVDKSRMQGNVFCSVNHEALNHNHYTKSLSPGK 452
```

RESULT 3

```
US-09-026-985-71
: Sequence 71, Application US/09026985
: Patent No. 613426
: GENERAL INFORMATION:
: APPLICANT: Gonzalez, Tania R.
: APPLICANT: Leong, Steven R.
: APPLICANT: Presta, Leonard G.
: TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
: TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatlin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/026,985
: FILING DATE: 20-Feb-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
```

REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P1085R3-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5530
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-09-026-985-71

Query Match 87.3%; Score 2193.5; DB 3; Length 452;
 Best Local Similarity 91.2%; Pred. No. 3.8e-170;
 Matches 417; Conservative 9; Mismatches 24; Indels 7; Gaps 2;

QY 20 EVQLLESGGGLVQPGSLRLSCAASGFTFSNTAMSVKROAPGKGLEWVAISAGHSTYL 79
 DB 1 EVQLVQSGGGLVQPGSLRLSCAASGYSFSSHYMHVROAPGKGLEWGYIDPSNGETTY 60
 QY 80 ADVSGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDEVTMIVLNGG--FDYWGOG 137
 DB 61 NQKFGRTLSRDNKNTAYLQMNSLRAEDTAVYYCARGD----YRYNGDWFFDYWGOG 115
 QY 138 TRFTVSSASTKGSPVFPLAPSSKSTSGGTAALGCLVKDYFPEPVYTWMSNGALTSGVHFE 197
 DB 116 TLVTYSSASTKSPVFPLAPSSKSTSGGTAALGCLVKDYFPEPVYTWMSNGALTSGVHFE 175
 QY 198 PAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHRKPSNTRVDKRVKPCSDKTHTCPPCP 257
 DB 176 PAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHRKPSNTRVDKRVKPCSDKTHTCPPCP 235
 QY 258 APELLGGPSVFLPPEPKKDTLMISRPPEYTCVVDVSHEDPEVKFMYVDGVEVHNAKTR 317
 DB 236 APELLGGPSVFLPPEPKKDTLMISRPPEYTCVVDVSHEDPEVKFMYVDGVEVHNAKTR 295
 QY 318 PREEOYNSTYRVVSVLTVLDHOMLNGEKYCKVSNKALPAPIEKTSKAKGQPREPQVYT 377
 DB 296 PREEOYNSTYRVVSVLTVLDHOMLNGEKYCKVSNKALPAPIEKTSKAKGQPREPQVYT 355
 QY 378 LPPSRDEMTKNQVSLTCLVKGFFPSDIAVEMESNGCPENNYKTTTPVLDSDGSFFLYSKL 437
 DB 356 LPPSRDEMTKNQVSLTCLVKGFFPSDIAVEMESNGCPENNYKTTTPVLDSDGSFFLYSKL 415
 QY 438 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPCK 474
 DB 416 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPCK 452

RESULT 4

US-09-121-952A-71
 Sequence 71, Application US/09121952A
 Patent No. 6458355
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc., Hsai, Vanessa
 APPLICANT: Koumenis, Iphigenia
 APPLICANT: Leong, Steven R.
 APPLICANT: Presta, Leonard G.
 APPLICANT: Shahrokh, Zahra
 APPLICANT: Zapata, Gerardo A.
 TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
 TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/121,952A
 FILING DATE: 24-JUL-1998
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/074330
 FILING DATE: 22-JAN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/075467
 FILING DATE: 20-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P1085R4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5530
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-09-121-952A-71

Query Match 87.3%; Score 2193.5; DB 4; Length 452;
 Best Local Similarity 91.2%; Pred. No. 3.8e-170;
 Matches 417; Conservative 9; Mismatches 24; Indels 7; Gaps 2;

QY 20 EVQLLESGGGLVQPGSLRLSCAASGFTFSNTAMSVKROAPGKGLEWVAISAGHSTYL 79
 DB 1 EVQLVQSGGGLVQPGSLRLSCAASGYSFSSHYMHVROAPGKGLEWGYIDPSNGETTY 60
 QY 80 ADVSGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDEVTMIVLNGG--FDYWGOG 137
 DB 61 NQKFGRTLSRDNKNTAYLQMNSLRAEDTAVYYCARGD----YRYNGDWFFDYWGOG 115
 QY 138 TRFTVSSASTKGSPVFPLAPSSKSTSGGTAALGCLVKDYFPEPVYTWMSNGALTSGVHFE 197
 DB 116 TLVTYSSASTKSPVFPLAPSSKSTSGGTAALGCLVKDYFPEPVYTWMSNGALTSGVHFE 175
 QY 198 PAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHRKPSNTRVDKRVKPCSDKTHTCPPCP 257
 DB 176 PAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHRKPSNTRVDKRVKPCSDKTHTCPPCP 235
 QY 258 APELLGGPSVFLPPEPKKDTLMISRPPEYTCVVDVSHEDPEVKFMYVDGVEVHNAKTR 317
 DB 236 APELLGGPSVFLPPEPKKDTLMISRPPEYTCVVDVSHEDPEVKFMYVDGVEVHNAKTR 295
 QY 318 PREEOYNSTYRVVSVLTVLDHOMLNGEKYCKVSNKALPAPIEKTSKAKGQPREPQVYT 377
 DB 296 PREEOYNSTYRVVSVLTVLDHOMLNGEKYCKVSNKALPAPIEKTSKAKGQPREPQVYT 355
 QY 378 LPPSRDEMTKNQVSLTCLVKGFFPSDIAVEMESNGCPENNYKTTTPVLDSDGSFFLYSKL 437
 DB 356 LPPSRDEMTKNQVSLTCLVKGFFPSDIAVEMESNGCPENNYKTTTPVLDSDGSFFLYSKL 415
 QY 438 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPCK 474
 DB 416 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPCK 452

RESULT 5

US-09-234-340A-71
 Sequence 71, Application US/09234340A
 Patent No. 6468532
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc., Hsai, Vanessa
 APPLICANT: Koumenis, Iphigenia
 APPLICANT: Leong, Steven R.
 APPLICANT: Presta, Leonard G.
 APPLICANT: Shahrokh, Zahra

APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipaln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-71

Query Match 87.3%; Score 2193.5; DB 4; Length 452;
Best Local Similarity 91.2%; Pred. No. 3.8e-170;
Matches 417; Conservative 9; Mismatches 24; Indels 7; Gaps 2;

QY 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVQAQPGKLEWYSAISAGSHSTYL 79
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSFHHMHWVQAQPGKLEWGYIDPSNGETTY 60
QY 80 ADVKGRFTISRDNKSKNTLYLQMSLRAEDTAVVYCAKDRVMTIVLNGG--PDYWGOG 137
DB 61 NQKRGRTISRDNKSKNTAYLQMSLRAEDTAVVYCAKDRVMTIVLNGG--PDYWGOG 115
QY 138 TRTVVSSASTKGPVFLPAPSSKSTSGGTALGLVNDKPEPYVSWNSGALTSGVHTF 197
DB 116 TLTVVSSASTKGPVFLPAPSSKSTSGGTALGLVNDKPEPYVSWNSGALTSGVHTF 175
QY 198 PAVLQSSGLVLSVSVYVSSSLGTQTYICNVNHPSTKVKDKRVEPKSCCKTRHCPCP 257
DB 176 PAVLQSSGLVLSVSVYVSSSLGTQTYICNVNHPSTKVKDKRVEPKSCCKTRHCPCP 235
QY 258 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDQEVHNATK 317
DB 236 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDQEVHNATK 295
QY 318 PREBOYNSTYRVSVLVTHQDMLNGKEKCKVSKALPARIETKISKAKGQPREPQVYT 377
DB 296 PREBOYNSTYRVSVLVTHQDMLNGKEKCKVSKALPARIETKISKAKGQPREPQVYT 355
QY 378 LPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 437
DB 356 LPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 415

QY 438 TVDKSRMOQGVNFCSCVHHEALHNHYTQKSLSPGK 474
DB 416 TVDKSRMOQGVNFCSCVHHEALHNHYTQKSLSPGK 452

RESULT 6
US-08-487-550-8
Sequence 8, Application US/08487550
Patent No. 6113698
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-8

Query Match 86.8%; Score 2183; DB 3; Length 478;
Best Local Similarity 86.7%; Pred. No. 2.9e-169;
Matches 418; Conservative 18; Mismatches 34; Indels 12; Gaps 3;

QY 1 MEGFLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVQAQ 60
DB 1 MGSWLLFLFLVAVVTRVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVQAQ 60
QY 61 GKGLEWYSAI--SASGHSFTYLAQSGKFTISRDNKSKNTLYLQMSLRAEDTAVVYCAK 118
DB 61 GKGLEWYSAI--SASGHSFTYLAQSGKFTISRDNKSKNTLYLQMSLRAEDTAVVYCAK 118
QY 119 REVMTIVLNGG-----FDYWGOGTRVTVSSASTKGPVFLPAPSSKSTSGGTALGLCL 172
DB 119 --TSVISHCRGVCYCGYFEEFGGALTVTSASSTKGPVFLPAPSSKSTSGGTALGLCL 176
QY 173 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVSSSLGTQTYICNVNHP 232
DB 173 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVSSSLGTQTYICNVNHP 236
QY 233 PSNTRKVDKRVPRKSDKTHHTPCRPAPRLLAGPSVFLFPPKPKDTLMISRTPEVTCVVVD 292
DB 237 PSNTRKVDKRVPRKSDKTHHTPCRPAPRLLAGPSVFLFPPKPKDTLMISRTPEVTCVVVD 296
QY 293 VSHEDPEVKFNWYVDQEVHNATKPREBOYNSTYRVSVLVTHQDMLNGKEKCKVSK 352

Db 297 VSHEDPEVKFNNYVGVGVHNAKTKPREQVNSTYRVSV.LVLHODMLNGKEYCKYSN 356
QY 333 KALPAPIEKTISKAKGQPREPOVYTLPPSRHEMTRKNQVSLCIVKGFFPSDIAVEMESNG 412
Db 357 KALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNG 416
QY 413 QPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQOGNVFSCVYMHEALHNHYTQKSLSLSP 472
Db 417 QPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQOGNVFSCVYMHEALHNHYTQKSLSLSP 476
QY 473 GK 474
Db 477 GK 478

RESULT 7
US-09-526-098-8
; Sequence 8, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATTHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526, 098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-8

Query Match 86.8%; Score 2183; DB 4; Length 478;
Best Local Similarity 86.7%; Pred. No. 2.9e-169;
Matches 418; Conservative 18; Mismatches 34; Indels 12; Gaps 3;

QY 1 MEFGSLPLVLAILEKVOCEVOGLLESGGLVOPGSLRLSCAAGFTFSNTYAMSVMVRAP 60
Db 1 MGRSLILPLVAVATRVOCVVOGLVOPGSLRLSCAAGFTFSNTYAMSVMVRAP 60
QY 61 GKLEWVAI--SASGHSTYLADSVKGRFTISRDSKNTLYLQMSLRAEDTAVVYCAKD 118
||| ||| | : : | ||| ||||| :||| :||| :||| |||||

Db 61 GKLEWVAIIRNKPNGTTEYASVYKDRFTISRDSKSLA.LQMSLKIETDIAVYYCT-- 118
QY 119 REYTMIVLNG-----FDYWGQTRVTVSSASTKGPVPLAPSSKTSCTGTAALGCL 172
Db 119 --TSYISHCGRGVCYGYFEFWGQALVTVSSASTKGPVPLAPSSKTSCTGTAALGCL 176
QY 173 VKDYFPEPTVSMNSGALISGVHTFPAYLQSSGLVLSGVTVVPSSLSGTQYICNVNKK 232
Db 177 VADYFPEPTVSMNSGALISGVHTFPAYLQSSGLVLSGVTVVPSSLSGTQYICNVNKK 236
QY 233 PSNTRVDRKRPKSCDKTHTPCPAPALGLGSPVFLPFPPLKDTLMSRTEPVTCVVD 292
Db 237 PSNTRVDRKRPKSCDKTHTPCPAPALGLGSPVFLPFPPLKDTLMSRTEPVTCVVD 296
QY 293 VSHEDPEVKFNNYVGVGVHNAKTKPREQVNSTYRVSV.LVLHODMLNGKEYCKYSN 352
Db 297 VSHEDPEVKFNNYVGVGVHNAKTKPREQVNSTYRVSV.LVLHODMLNGKEYCKYSN 356
QY 353 KALPAPIEKTISKAKGQPREPOVYTLPPSRHEMTRKNQVSLCIVKGFFPSDIAVEMESNG 412
Db 357 KALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLCIVKGFFPSDIAVEMESNG 416
QY 413 QPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQOGNVFSCVYMHEALHNHYTQKSLSLSP 472
Db 417 QPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQOGNVFSCVYMHEALHNHYTQKSLSLSP 476
QY 473 GK 474
Db 477 GK 478

RESULT 8
US-09-679-397-2
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241RID2
; CURRENT FILING DATE: 2000-10-03
; CURRENT APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-09-679-397-2

Query Match 86.8%; Score 2181.5; DB 4; Length 449;
Best Local Similarity 90.6%; Pred. No. 3.5e-169;
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

QY 20 EVQLLESGGGLVQPGSLRLSCAAGFTFSNTYAMSVMVRQIPKGLIEWVAISASGHSTYL 79
Db 1 EVQLVESGGGLVQPGSLRLSCAAGFTFSNTYAMSVMVRQIPKGLIEWVAIRIPTNGYTRY 60
QY 80 ADVYKGRFTISRDSKNTLYLQMSLRAEDTAVVYCAKDIEVYTMIVLNG-----FDYW 134
Db 61 ADVYKGRFTISRDSKNTLYLQMSLRAEDTAVVYCSR-----WGCGGFYAMDYW 110
QY 135 GGGTAVTVSSASTKGPVPLAPSSKTSCTGTAALGCLVDYFPEPTVSMNSGALTSGV 194
Db 111 GGGTAVTVSSASTKGPVPLAPSSKTSCTGTAALGCLVDYFPEPTVSMNSGALTSGV 170
QY 195 HFPVAVLQSSGLYSLSVTVVPSSLSGTQYICNVNKKRPNKRVKRPKCDKTHNCP 254
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 171 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQTYICNVNHRPSNTKYDKKVEPKSCDKTHTCP 230
Qy 255 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDDGEVHNA 314
Db 231 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDDGEVHNA 290
Qy 315 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 374
Db 291 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 350
Qy 375 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNNKTPPVLDSDGSFFLY 434
Db 351 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNNKTPPVLDSDGSFFLY 410
Qy 435 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 473
Db 411 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 449

RESULT 9
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D1
; CURRENT APPLICATION NUMBER: US/09/680,148
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
US-09-680-148-2

Query Match 86.8%; Score 2181.5; DB 4; Length 449;
Best Local Similarity 90.6%; Pred. No. 3,5e-169;
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

Qy 20 EVQLLEGGGGLVQPGSLRLSQAASGFTFSNYAMSWRQAPGKLEWVAISASGHSTYL 79
Db 1 EVQLVESGGGLYQPGGSLRLSQAASGFNIKDTYIHWVROAPGKLEWVARIYPTNGYTRY 60
Qy 80 ADSVKGRFTISRDNSKNTLYLQMNSLRADPAVAYVYCAKDRVMTIIVLNGS----FDYW 134
Db 61 ADSVKGRFTISADTSKNTATLQMNSLRADPAVAYVYCSR-----WGSDGFYAMDYW 110
Qy 135 GGGTRVTVSSASTGSPVFLPAPSSKSTSGGTALGCLVYKDPPEPYTVSNNGALTSV 194
Db 111 GGGTLVTVSSASTGSPVFLPAPSSKSTSGGTALGCLVYKDPPEPYTVSNNGALTSV 170
Qy 195 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQTYICNVNHRPSNTKYDKKVEPKSCDKTHTCP 254
Db 171 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQTYICNVNHRPSNTKYDKKVEPKSCDKTHTCP 230
Qy 255 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDDGEVHNA 314
Db 231 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDDGEVHNA 290
Qy 315 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 374
Db 291 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 350
Qy 375 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNNKTPPVLDSDGSFFLY 434
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Db 351 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNNKTPPVLDSDGSFFLY 410
Qy 435 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 473
Db 411 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 449

RESULT 10
US-09-304-465A-2
; Sequence 2, Application US/09304465A
; Patent No. 6489447
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1
; CURRENT APPLICATION NUMBER: US/09/304,465A
; CURRENT FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6489447
US-09-304-465A-2

Query Match 86.8%; Score 2181.5; DB 4; Length 449;
Best Local Similarity 90.6%; Pred. No. 3,5e-169;
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

Qy 20 EVQLLEGGGGLVQPGSLRLSQAASGFTFSNYAMSWRQAPGKLEWVAISASGHSTYL 79
Db 1 EVQLVESGGGLYQPGGSLRLSQAASGFNIKDTYIHWVROAPGKLEWVARIYPTNGYTRY 60
Qy 80 ADSVKGRFTISRDNSKNTLYLQMNSLRADPAVAYVYCAKDRVMTIIVLNGS----FDYW 134
Db 61 ADSVKGRFTISADTSKNTATLQMNSLRADPAVAYVYCSR-----WGSDGFYAMDYW 110
Qy 135 GGGTRVTVSSASTGSPVFLPAPSSKSTSGGTALGCLVYKDPPEPYTVSNNGALTSV 194
Db 111 GGGTLVTVSSASTGSPVFLPAPSSKSTSGGTALGCLVYKDPPEPYTVSNNGALTSV 170
Qy 195 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQTYICNVNHRPSNTKYDKKVEPKSCDKTHTCP 254
Db 171 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQTYICNVNHRPSNTKYDKKVEPKSCDKTHTCP 230
Qy 255 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDDGEVHNA 314
Db 231 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDDGEVHNA 290
Qy 315 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 374
Db 291 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 350
Qy 375 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNNKTPPVLDSDGSFFLY 434
Db 351 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNNKTPPVLDSDGSFFLY 410
Qy 435 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 473
Db 411 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 449

RESULT 11
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
```

APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39, 044
REFERENCE/DOCKET NUMBER: P0718P2CID1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-8

Query Match 86.6%; Score 2178; DB 3; Length 453;
Best Local Similarity 90.8%; Pred. No. 6,9e-169;
Matches 416; Conservative 14; Mismatches 20; Indels 8; Gaps 4;

QY 20 EVQLLESGGGLVQPQGSRLSCAASGFTF-SNYAMSWVQAQPGKLEWVAISASGHSY 78
DB 1 EVQLVESGGGLVQPGSLRLSCAASGYSITSGYSNMWIMQAPGKLEWVAISITYGSTNY 60

QY 79 LADSVKGRFTISRDNKSKNTLYIQMNSLRAEDTAVYYCAKRDREYTMIVLNGGFDYWGOST 138
DB 61 -ADSVKGRFTISRDNKSKNTFYLMNNSLRAEDTAVYYCANGSH---YFGHMFAVWGOST 115

QY 139 RYTVASAST--KGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHT 196
DB 116 LVTYVSASTKKGKGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHT 175

QY 197 FPAVLQSSGLYSLSVTVPPSSSLGTQTYICVNNHNPSTKYDKRVEPKSCDTHTCPPC 256
DB 176 FPAVLQSSGLYSLSVTVPPSSSLGTQTYICVNNHNPSTKYDKRVEPKSCDTHTCPPC 235

QY 257 PAPELLGPSVFLFPKPKDITMISRTPEVTCVVDVSHDEPKVFNMTVDGEVYNAKT 316
DB 236 PAPELLGPSVFLFPKPKDITMISRTPEVTCVVDVSHDEPKVFNMTVDGEVYNAKT 295

QY 317 KPREDQYNSTYRVSVLTVLHDQWLNGKRYKCKVSNKALPAPIEKTISAKGQPREPQY 376

|||||
DB 296 KPREDQYNSTYRVSVLTVLHDQWLNGKRYKCKVSNKALPAPIEKTISAKGQPREPQY 355

QY 377 TLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNQGPENNTKTPPVLDSDGSFFLYSK 436
DB 356 TLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNQGPENNTKTPPVLDSDGSFFLYSK 415

QY 437 LTVDKSRMQGVNFCVSNVHEALHNHYTQKSLSLSPGK 471
DB 416 LTVDKSRMQGVNFCVSNVHEALHNHYTQKSLSLSPGK 453

RESULT 12
US-08-466-163B-8
Sequence 8, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2CID1
CURRENT APPLICATION NUMBER: US/08/466,163B
FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 8
LENGTH: 453
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: humanized maell, version 1 heavy/chain
US-08-466-163B-8

Query Match 86.6%; Score 2178; DB 4; Length 453;
Best Local Similarity 90.8%; Pred. No. 6,9e-169;
Matches 416; Conservative 14; Mismatches 20; Indels 8; Gaps 4;

QY 20 EVQLLESGGGLVQPQGSRLSCAASGFTF-SNYAMSWVQAQPGKLEWVAISASGHSY 78
DB 1 EVQLVESGGGLVQPGSLRLSCAASGYSITSGYSNMWIMQAPGKLEWVAISITYGSTNY 60

QY 79 LADSVKGRFTISRDNKSKNTLYIQMNSLRAEDTAVYYCAKRDREYTMIVLNGGFDYWGOST 138
DB 61 -ADSVKGRFTISRDNKSKNTFYLMNNSLRAEDTAVYYCANGSH---YFGHMFAVWGOST 115

QY 139 RYTVASAST--KGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHT 196
DB 116 LVTYVSASTKKGKGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHT 175

QY 197 FPAVLQSSGLYSLSVTVPPSSSLGTQTYICVNNHNPSTKYDKRVEPKSCDTHTCPPC 256
DB 176 FPAVLQSSGLYSLSVTVPPSSSLGTQTYICVNNHNPSTKYDKRVEPKSCDTHTCPPC 235

QY 257 PAPELLGPSVFLFPKPKDITMISRTPEVTCVVDVSHDEPKVFNMTVDGEVYNAKT 316
DB 236 PAPELLGPSVFLFPKPKDITMISRTPEVTCVVDVSHDEPKVFNMTVDGEVYNAKT 295

QY 317 KPREDQYNSTYRVSVLTVLHDQWLNGKRYKCKVSNKALPAPIEKTISAKGQPREPQY 376
DB 296 KPREDQYNSTYRVSVLTVLHDQWLNGKRYKCKVSNKALPAPIEKTISAKGQPREPQY 355

QY 377 TLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNQGPENNTKTPPVLDSDGSFFLYSK 436
DB 356 TLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNQGPENNTKTPPVLDSDGSFFLYSK 415

QY 437 LTVDKSRMQGVNFCVSNVHEALHNHYTQKSLSLSPGK 474

Db 416 LTVDKSRMOGQGNVFCSCVMHEALHNHYTKSLSPGK 453

RESULT 13

US-08-887-352B-18
; Sequence 18, Application US/08887352B
; Patent No. 5994511

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,352B

FILING DATE: 03-Jul-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P1123

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-887-352B-18

Query Match 86.4%; Score 2173; DB 2; Length 451;
Best Local Similarity 90.8%; Pred. No. 1.7e-168;

Matches 414; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

Db 20 EVOLLESGGLVOPGGSRLSCASGTF-SNYAMSWROAPRGLEWVASIASGHTY 78

Db 1 EVOLVESGGGLVOPGGSRLSCASGTSITSGYSNMWIRAPRGLEWVASIKYSGETKY 60

QY 79 LADSVKGRFTISRDNKNTLYLQNMNSLAEDTAVAYYCAKDREVTMIVLNGCFDYWGOGT 138

Db 61 -NPSVKGRFTISRDNKNTLYLQNMNSLAEDTAVAYYCAKRSRSH---YGHMHPFVWVGOGT 115

QY 139 RVTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 198

Db 116 LVTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 175

QY 199 AVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHRPSNKKVDKKEPKSCDTHTCPCPPA 258

Db 176 AVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHRPSNKKVDKKEPKSCDTHTCPCPPA 235

QY 259 PELLGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNATKP 318

Db 236 PELLGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNATKP 295

QY 319 REEOYNSTYRVVSVLTVLHDQMLNGKEYKKCKVSKALPAPIEKTISKAKGPRRPQVYTL 378

Db 296 REEOYNSTYRVVSVLTVLHDQMLNGKEYKKCKVSKALPAPIEKTISKAKGPRRPQVYTL 355

QY 379 PPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 438

Db 379 PPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 438

Db 356 PPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 415

QY 439 VDKSRMOGQGNVFCSCVMHEALHNHYTKSLSPGK 474

Db 416 VDKSRMOGQGNVFCSCVMHEALHNHYTKSLSPGK 451

RESULT 14

US-09-109-207C-18
; Sequence 18, Application US/09109207C
; Patent No. 6172213

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept

FILE REFERENCE: P1123R1

CURRENT APPLICATION NUMBER: US/09/109,207C

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/051,554

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 18

LENGTH: 451

TYPE: PRT

ORGANISM: Artificial

FEATURE:

NAME/KEY: Artificial

LOCATION: 1-451

OTHER INFORMATION: Heavy chain sequence derived from MAE11

US-09-109-207C-18

Query Match 86.4%; Score 2173; DB 3; Length 451;
Best Local Similarity 90.8%; Pred. No. 1.7e-168;

Matches 414; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 20 EVOLLESGGLVOPGGSRLSCASGTF-SNYAMSWROAPRGLEWVASIASGHTY 78

Db 1 EVOLVESGGGLVOPGGSRLSCASGTSITSGYSNMWIRAPRGLEWVASIKYSGETKY 60

QY 79 LADSVKGRFTISRDNKNTLYLQNMNSLAEDTAVAYYCAKDREVTMIVLNGCFDYWGOGT 138

Db 61 -NPSVKGRFTISRDNKNTLYLQNMNSLAEDTAVAYYCAKRSRSH---YGHMHPFVWVGOGT 115

QY 139 RVTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 198

Db 116 LVTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 175

QY 199 AVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHRPSNKKVDKKEPKSCDTHTCPCPPA 258

Db 176 AVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHRPSNKKVDKKEPKSCDTHTCPCPPA 235

QY 259 PELLGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNATKP 318

Db 236 PELLGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNATKP 295

QY 319 REEOYNSTYRVVSVLTVLHDQMLNGKEYKKCKVSKALPAPIEKTISKAKGPRRPQVYTL 378

Db 296 REEOYNSTYRVVSVLTVLHDQMLNGKEYKKCKVSKALPAPIEKTISKAKGPRRPQVYTL 355

QY 379 PPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 438

Db 356 PPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 415

QY 439 VDKSRMOGQGNVFCSCVMHEALHNHYTKSLSPGK 474

Db 416 VDKSRMOGQGNVFCSCVMHEALHNHYTKSLSPGK 451

RESULT 15

US-09-282-505-2

; Sequence 2, Application US/09282505A

; Patent No. 6194551

GENERAL INFORMATION:

APPLICANT: Esche Eklinaduse Idusogie et al.

; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-2

Query Match 86.4%; Score 2173; DB 3; Length 451;
Best Local Similarity 90.8%; Pred. No. 1.7e-168;
Matches 414; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

OY 20 EVQLLEGGGLVOPGSGRLSCAASGTF-SNYAMSWVRQAPGKLEWVASISAGHSTY 78
DB 1 EVQLVESGGGLVQPGSLRLSCAASGYSITSGYSNMWIRQAPGKLEWVASIKYSGETKY 60
OY 79 LADSVKGRFTISRDNKNTLYIQMNSLRAPETAAYVYCAKDRVETMIIVLNGGFDYWGQGT 138
DB 61 -NPSYKGRITISRDNKNTLYIQMNSLRAPETAAYVYCAKDRVETMIIVLNGGFDYWGQGT 115
OY 139 RVTYSSASTKGPSPVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 198
DB 116 LVTYSSASTKGPSPVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 175
OY 199 AVLOSGLYSLSVYTVSSSLGTQTYICNNHKSNTKVDKRVPEPKSCDKTHTCPCPA 258
DB 176 AVLOSGLYSLSVYTVSSSLGTQTYICNNHKSNTKVDKRVPEPKSCDKTHTCPCPA 235
OY 259 PELTGGPSVFLEPPPKDITLMSRPEVTCVYVDYSHEDPEYKFMNMYVDGVEVHNAKTRP 318
DB 236 PELTGGPSVFLEPPPKDITLMSRPEVTCVYVDYSHEDPEYKFMNMYVDGVEVHNAKTRP 295
OY 319 REEOYNSTYRVSVVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 378
DB 296 REEOYNSTYRVSVVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 355
OY 379 PPSREEMTKNOVSLTCLVKGFPYSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLT 438
DB 356 PPSREEMTKNOVSLTCLVKGFPYSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLT 415
OY 439 VDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 474
DB 416 VDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 451

Search completed: September 12, 2003, 13:05:13
Job time : 28.7797 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:56:44; Search time 82.3475 Seconds
(without alignments)
1485.376 Million cell updates/sec

Title: US-09-848-832-3

Perfect score: 2514
Sequence: 1 MEFGLSMFLVAILKGYCE.....MHEALHNHTOKSLSPCK 474

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL.23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2325.5	92.5	471	4	Q8TC77
2	2105.5	83.8	521	4	Q8N4Y9
3	1882	74.9	473	4	Q8TC63
4	1660.5	66.1	469	11	Q8R3V9
5	1625.5	64.7	509	4	Q8NFI7
6	1587.5	63.1	473	11	Q91Z05
7	1541.5	60.1	437	11	Q9R1A4
8	1511.5	59.5	463	11	Q9D8L4
9	1495.5	57.5	468	11	Q991C4
10	1474	58.6	473	11	Q991C3
11	1446.5	56.2	473	11	Q991C2
12	1414	55.0	474	11	Q8R3H6
13	1263.5	50.3	337	6	Q95M34
14	1257	50.0	701	4	Q96F08
15	1061.5	42.2	597	4	Q96B89
16	1010	40.2	613	4	Q8WUK1

17	929	37.0	494	4	Q96K68	Q96K68 homo sapien
18	926.5	36.9	499	4	Q8N5K4	Q8N5K4 homo sapien
19	907.5	36.1	493	4	Q8NCL6	Q8NCL6 homo sapien
20	897.5	35.7	467	11	Q99KA4	Q99KA4 mus musculu
21	866.5	34.5	479	11	Q91WP5	Q91WP5 mus musculu
22	846	33.7	486	11	Q91Z07	Q91Z07 mus musculu
23	822.5	32.7	480	11	Q91XE1	Q91XE1 mus musculu
24	811	32.3	484	11	Q8VEA0	Q8VEA0 mus musculu
25	775	30.8	573	4	Q8WU38	Q8WU38 homo sapien
26	757	30.1	613	11	Q8VCX7	Q8VCX7 mus musculu
27	755.5	30.1	597	4	Q9BU10	Q9BU10 homo sapien
28	755	30.0	278	11	Q921K1	Q921K1 mus musculu
29	754.5	30.0	614	4	Q96GA6	Q96GA6 homo sapien
30	753.5	30.0	597	4	Q9BDB8	Q9BDB8 homo sapien
31	746	29.7	613	4	Q96EX0	Q96EX0 homo sapien
32	745.5	29.7	588	4	Q8WUX4	Q8WUX4 homo sapien
33	745.5	29.7	618	4	Q96AA6	Q96AA6 homo sapien
34	724	28.8	500	4	Q9BRV0	Q9BRV0 homo sapien
35	702.5	27.9	497	4	Q8WY24	Q8WY24 homo sapien
36	701	27.9	484	11	Q99LA6	Q99LA6 mus musculu
37	697.5	27.7	481	11	Q91WT1	Q91WT1 mus musculu
38	692	27.5	482	11	Q91X92	Q91X92 mus musculu
39	692	27.5	496	4	Q96DK0	Q96DK0 homo sapien
40	691	27.5	482	11	Q8K172	Q8K172 mus musculu
41	687	27.3	480	11	Q8K0Z4	Q8K0Z4 mus musculu
42	681	27.1	486	4	Q96KX8	Q96KX8 homo sapien
43	678	26.8	488	11	Q8K0F2	Q8K0F2 mus musculu
44	673.5	26.8	489	11	Q8VCX4	Q8VCX4 mus musculu
45	670	26.7	488	11	Q91WR1	Q91WR1 mus musculu

ALIGNMENTS

RESULT 1

ID	Q8TC77	PRELIMINARY:	PRT:	471 AA.
AC	Q8TC77			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RA	Strausberg R.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC024289; AAH24289.1; -			
DR	InterPro: IPR007110; Ig_Like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig; 4.			
DR	SMART: SM00406; Ig; 1.			
DR	PROSITE: PS50835; IG_LIKE; 4.			
DR	PROSITE: PS00290; IG_MHC; 2.			
KW	Hypothetical protein			
SQ	SEQUENCE 471 AA; 51791 MW; 3887F4CF588660E C'RC64;			

Query Match 92.5%; Score 2325.5; DB 4; Length 471;
Best Local Similarity 92.2%; Pred. No. 2.2e-183;
Matches 438; Conservative 19; Mismatches 13; Indels 5; Gaps 2;

Qy	1	MEFGLSMFLVAILKGYCEVQLLESGGGLVGGGSLRLS;AASGFTFSYNAASWYRQAP 60
Db	1	MEFGLSMFLVAILKGYCEVQLLESGGGLVGGGSLRLS;AASGFTFSYNAASWYRQAP 60
Qy	61	GKLEWVASIASGSHSTYLAADVSKGRFTISRDNKNTLY;JNMSLAEDPAVYCKAD-R 119
Db	61	GKLEWVASIASGSHSTYLAADVSKGRFTISRDNKNTLY;JNMSLAEDPAVYCKAD-R 120

QY	120	EVMTMLVVLNGGPDVYACGGRVTVSSASTGSPVFLPABSPKSTSGGTAALGCLVKQDPE	179
		QITISWY----FDLNGKGLTVVSSASTKGPSPFLPABSPKSTSGGTAALGCLVKQYFPE	176
Db	121	QITISWY----FDLNGKGLTVVSSASTKGPSPFLPABSPKSTSGGTAALGCLVKQYFPE	176
QY	180	PVTVSMNSGALITSGVHTPEPAVLQSSGLVSLSSVVTIPSSSLGTQTYICVNHKPSMTKYD	239
Db	177	PVTVSMNSGALITSGVHTPEPAVLQSSGLVSLSSVVTIPSSSLGTQTYICVNHKPSMTKYD	236
QY	240	KRVKPSGDKTHTCPCPCAPPELLGGSPVLFPPKPKDPTLMISTPEVTCVYVYSHEDPE	299
Db	237	KRVKPSGDKTHTCPCPCAPPELLGGSPVLFPPKPKDPTLMISTPEVTCVYVYSHEDPE	296
QY	300	VKFNMYVDGVEVHNAAKTPREBOQYNSTYRVASVLYLVHODWLNKGEYKCKVSKNALPAPI	359
Db	297	VKFNMYVDGVEVHNAAKTPREBOQYNSTYRVASVLYLVHODWLNKGEYKCKVSKNALPAPI	356
QY	360	EKTIKAKGPREPQVYTLTPRSREEMTKNQVSLTCTCVKGFYPSDIAVEMENSGQPENNK	419
Db	357	EKTIKAKGPREPQVYTLTPRSREDELTKNQVSLTCTCVKGFYPSDIAVEMENSGQPENNK	416
QY	420	TTTPVLDSDGSEFFLYSKLTVDKSRMQGQVNFSCSVNHEALAHNHYYTOKSLSLSPGK	474
Db	417	TTTPVLDSDGSEFFLYSKLTVDKSRMQGQVNFSCSVNHEALAHNHYYTOKSLSLSPGK	471

RESULT 2	
Q8N4Y9	PRELIMINARY; PRT; 521 AA.
ID Q8N4Y9	
AC Q8N4Y9;	
DT 01-OCT-2002 (TREMBL; 22, Created)	
DT 01-OCT-2002 (TREMBL; 22, Last sequence update)	
DT 01-MAR-2003 (TREMBL; 23, Last annotation update)	
DE Hypothetical protein.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA TISSUE=Primary B-cells from Tonsils;	
RA Straussberg R.;	
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.	
DR EMBL: BC033178; ANH33178.1; -	
DR InterPro: IPR007110; Ig_Like.	
DR InterPro: IPR003597; Ig_CL.	
DR InterPro: IPR003006; Ig_MHC.	
DR InterPro: IPR003596; Ig_V.	
DR Pfam: PF00047; Ig_4.	
DR SMART: SM00407; IGCL1.3.	
DR SMART: SM00406; IGV.1.	
DR PROSITE: PS00835; IG_LIKE; 4.	
DR PROSITE: PS00290; IG_MHC; 2.	
DR Hypothetical protein.	
Q8 SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CA2A2 CRC64;	

Query Match	83.8%;	Score 2105.5;	DB 4;	Length 521;
Best Local Similarity	77.28;	Pred. No. 3.6e-165;		
Matches 404;	Conservative 26;	Mismatches 42;	Indels 51;	Gaps 3

[illegible]

Db	179	EPVYTSWNSGALTSQVHTPPAVLQSSGLXLSSSVYTPVSSSLCTQTYYTCNVHNHKKPENTKY	238
QY	239	DKRV-----	EBKSCDKTH 251
Db	239	DKRVELKPTPLGDTHTCPRCPEPKSCDTPPCRCPEPKSCDTP	298
QY	252	TCPRCPEPBLGGPSVFLFRPKPKDTLMSIKRPEYTCVYVDVSHEDPEVKFNNYVGVGEY	311
Db	259	PCPRCPAEELGGPSVFLFRPKPKDTLMSIKRPEYTCVYVDVSHEDPEVKFNNYVGVGEY	358
QY	312	HNAAKKPREEOYNSTYRVYSVLYTLVHOMLNGKEVKCKYSNKALPAPIEKTISKAKGQPR	371
Db	359	HNAAKKPREEOQNSTFRVYSVLYTLVHOMLNGKEVKCKYSNKALPAPIEKTISKAKGQPR	418
QY	372	EPQVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVYLDSDGSF	431
Db	419	EPQVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESGQPENNYNTTPVYLDSDGSF	478
QY	432	FLYSKLTIVDKSRMOOGNVPFSGSVMEHALNHNHTQKSLSPCK	474
Db	479	FLYSKLTIVDKSRMOOGNVPFSGSVMEHALNHNHTQKSLSPCK	521

RESULT 3		
08TCC3	PRELIMINARY:	PRT: 473 AA.
ID	08TCC3	
AC	Q8TCC3;	
DC	01-JUN-2002 (TrEMBLrel. 21, Created)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	
DE	Hypothetical protein.	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Kidney;	
RA	Strausberg R.;	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC025985; AAH25985.1; -	
DR	InterPro: IPR000923; BlueCu.1.	
DR	InterPro: IPR003110; Ig-like.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	InterPro: IPR003596; Ig_V.	
DR	Pfam; PFE0047; Ig_4.	
DR	SMART; SM00406; IGV_1.	
DR	PROSITE; PS00196; COPPER_BLUE. 1.	
DR	PROSITE; PS00835; IG_LIKE. 4.	
DR	PROSITE; PS00290; IG_MHC. 3.	
DR	Hypothetical protein.	
QO	SEQUENCE 473 AA: 51986 MW; E29920B09BA369P5 CRC64;	

Query Match	74.9%;	Score 1882;	DB 4;	Length 473;
Best Local Similarity	77.8%;	Pred. No. 8.7e-147;		
Matches 368;	Conservative 31;	Mismatches 58;	Indels 16;	Gaps 6;

[illegible]

Query	Match	Best Local Similarity	Score	64.7%	1625.5	DB 4	Length	509	
Matches	309	Conservative	9	Mismatches	11	Indels	47	Gaps	1
QY	144	SASTGSPVFPPLAPSPKSGSTALGCLVKDYPPEPVYVWNSGALSGVHTPPAYLOS	203						
DB	63	AASIKGSPVFPPLAPSRSTSGGTALGCLVKDYPPEPVYVWNSGALSGVHTPPAYLOS	122						
QY	204	SGLYSLSSVYVPPSSSLGTQYICVWNHNPSTKTKDKRY	242						
DB	123	SGLYSLSSVYVPPSSSLGTQYICVWNHNPSTKTKDKRY	182						
QY	243	-----EPKSCDKTHTCPRIAPBELLGSPVTLFPKPKD	276						
DB	183	CDTPPCCPRCPERPKSCDTPPCCPRCPERPKSCDTPPCCPRCPRIAPBELLGSPVTLFPKPKD	242						
QY	277	TLMISRTPEVNCVVVDVSHEDPEVFNWYVDDVEVHNATKPREROYNTSTVYVSLTVL	336						
DB	243	TLMISRTPEVNCVVVDVSHEDPEVFNWYVDDVEVHNATKPREROYNTSTVYVSLTVL	302						
QY	337	HODMNGKREYKCKVSNKALPAIEIKTISKAKGQPEPOVYVLPSPREEMTKNOVSLTCLY	396						
DB	303	HODMNGKREYKCKVSNKALPAIEIKTISKAKGQPEPOVYVLPSPREEMTKNOVSLTCLY	362						
QY	397	KGYFSDIAVEMESNGQPEPNNTKTPPVYLDGSGFFLYSKLTVDKSRMOQGNVFGSVNH	456						
DB	363	KGYFSDIAVEMESNGQPEPNNTKTPPVYLDGSGFFLYSKLTVDKSRMOQGNVFGSVNH	422						
QY	457	EALHNHYTOKSLSLSP	472						
DB	423	EALHNHYTOKSLSLSP	438						

RESULT 6

Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010327; AA010327.1; -
DR MGI: 2144967; AU044919.
DR InterPro: IPR00345; CytC_heme_bind.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.1%; Score 1587.5; DB 11; Length 473;
Best Local Similarity 62.6%; Pred. No. 1.7e-122;
Matches 301; Conservative 70; Mismatches 95; Indels 15; Gaps 4;

QY 1 MEFLSMFLVAILKGVQCEVQLLESGGGLVQPGSGSLRSCAASGFTTSNAMSVMVRAP 60
DB 1 MDSRLNLFVLLKGVQCEVQLLESGGGLVQPGSGSLRSCAASGFTTSNAMSVMVRAP 60
QY 61 GKLEWWSAISASGSHSTLADSVKGRFTISDNKNTLYLQMSLRADETAVVYCAKRE 120
DB 61 EKGLEWWSAISASGSHSTLADSVKGRFTISDNKNTLYLQMSLRADETAVVYCAKRE 120
QY 121 VTMLVNLNGFDYWGQGTTRVTVSSASTKGPSVFPFLAPSSKSTSGTALGCLVNDYRPP 180
DB 121 LRRV-----DYWGQGTTRVTVSSASTKGPSVFPFLAPSSKSTSGTALGCLVNDYRPP 180
QY 181 VTVMWNSGALTSVHTPRAVLQSSGLVSLSVTVVPSSSLGTQYICNVNKRKPSATKDK 240
DB 174 VTVMWNSGALTSVHTPRAVLQSSGLVSLSVTVVPSSSLGTQYICNVNKRKPSATKDK 240
QY 241 RVEPRSCDKT-HTCP-----CPAPELLGSPSVFLFPKPKDTLMISRTPEVTCVYVD 293
DB 233 KLESGSPSTINPCRPCKCKCHKCAPNLGEGSPVIFPPNKKVDLMSLTSTKVCVYVD 292
QY 294 SHEPPEVKFMYVGVGEVYHNNAKTRPREQYINSTRVSVTLVLDHMDLNGEKYCKVSNK 353
DB 293 SEDPRDVISWFWNVNVEHTAQOTQTHREDYINSTRVSALEPQHDWMSGEKFKCVNKK 352
QY 354 ALPAPIETKSKAGQPREPOVYTLPPSREMTKNQVSLTCLVNGFYPSDIAVWESNGQ 413
DB 353 DLPSPRIETKSKILGLVRAPOVYTLPPRAEQLSKRVDLCTLVGFGNGDLSVETWSNGH 412
QY 414 PENNYKTPPYLDSDGSFFLYSKTLVDKSRWQGNVSCSVNHEALHNHYTKSLSPG 473
DB 413 TEENYKTPPYLDSDGSFFLYSKTLVDKSRWQGNVSCSVNHEALHNHYTKSLSPG 472
QY 474 K 474
DB 473 K 473

RESULT 7

Q9R1A4 PRELIMINARY; PRT; 437 AA.

AC Q9R1A4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv)."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152372; AAD40243.1; -
DR HSSP: P01842; 7FAB.
DR MGI: 96446; Igh-4.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;

Query Match 61.3%; Score 1541.5; DB 11; Length 437;
Best Local Similarity 63.0%; Pred. No. 9.7e-119;
Matches 288; Conservative 68; Mismatches 78; Indels 23; Gaps 7;

QY 21 VQLLESGGGLVQPGSGSLRSCAASGFTTSNAMSVMVRAPGKLEWWSAISASGSHSTYLA 80
DB 1 VQLLESGGGLVQPGSGSLRSCAASGFTTSNAMSVMVRAPGKLEWWSAISASGSHSTYLA 80
QY 81 DSVKGRFTISDNKNTLYLQMSLRADETAVVYCAKREVTMLVNLNGFD-YWGQGT 139
DB 60 DSVKGRFTIYKDKDRNLIISLQMSLRSEDYAMVYCAR-----GDYSAYWGPQT 108
QY 140 VTVMWNSGALTSVHTPRAVLQSSGLVSLSVTVVPSSSLGTQYICNVNKRKPSATKDK 199
DB 109 VTVMWNSGALTSVHTPRAVLQSSGLVSLSVTVVPSSSLGTQYICNVNKRKPSATKDK 198
QY 200 VLOSGGLVSLSVTVVPSSSLGTQYICNVNKRKPSATKDKRVEPRSCDKTHTCP--CP 257
DB 169 VLOSGD-LYTLSSSVTVPSSTWSPSEYVNCVNAHPASSFVVDKKIYPRDGG--CKPCICT 223
QY 258 APPELLGSPSVFLFPKPKDTLMISRTPEVTCVYVDVSHEDPEVKFMYVGVGEVYHNNAK 317
DB 224 VPEV--SSVPIFPKPKDVLITLTPKRVTVVVDISKDDEVOFSMVDVDEHTAQOT 280
QY 318 PREQYINSTRVSVTLVLDHMDLNGEKYCKVSNKALPAPIETKSKAGQPREPOVY 377
DB 281 PREQYINSTRVSVTLVLDHMDLNGEKYCKVSNKALPAPIETKSKAGQPREPOVY 376
QY 378 LPPSREMTKNQVSLTCLVNGFYPSDIAVWESNGENNYKTPPYLDSDGSFFLYSK 437
DB 341 IPPKEDQAKVKSGLTCTITFPREDITVEQWNGQGAENYKNKQPIIMDTGSGFYVSKL 400
QY 438 TVDKSRWQGNVSCSVNHEALHNHYTKSLSPG 474
DB 401 NVOKSNMEAGNTFTCSVLHLEGLHNHTEKNSHSPGK 437

RESULT 8

Q9D8L4 PRELIMINARY; PRT; 473 AA.

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AC 09D814:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE 1810060009Rik protein.
GN IGH-1 OR 1810060009Rik.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pancreas;
RX MEDLINE=21085660; PubMed=11217651;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochila H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayshtaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007918; BAB25349.1;
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR007110; Igh-1Ike.
DR InterPro: IPR003006; Iq_1Ike.
DR InterPro: IPR003596; Iq_v.
DR Pfam: PF00047; Iq; 4.
DR SMART: SM00406; Iq; 1.
DR PROSITE: PS50835; Iq_LIKE; 4.
DR PROSITE: PS00290; Iq_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 60.1%; Score 1511.5; DB 11; Length 473;
Best Local Similarity 57.1%; Pred. No. 3.2e-116;
Matches 277; Conservative 85; Mismatches 100; Indels 23; Gaps 4;

OY 1 MEGGLSMFLVAILKGVOCVOLLSSGGGLVPGGSLRLSCAASGFTFSNYAMSWYRQAP 60
DB 1 MEMSWFLFLISVTGAVHCVOLKOSGALVYKPGASVKISCKASGYTFDYINWKORP 60
OY 61 GGLGVNSAISAAGSTYLAADVSKGRFTISRDNSKNTLYIQMNSLRADFTAVYYCAKDE 120
DB 61 GGLGVNSAISAAGSTYLAADVSKGRFTISRDNSKNTLYIQMNSLRADFTAVYYCAKDE 120
OY 121 VMIIVVLNGGPD-----YMGCGTRVYSSASTKGPSPFLAPSSKSTSGTALGCLVND 175
DB 121 VMIIVVLNGGPD-----YMGCGTRVYSSASTKGPSPFLAPSSKSTSGTALGCLVND 175
OY 118 -----SGDYDMFAVYGQGLTVYSAAKTTAPSVYPLAPVCGGTSSVTLGCLVAG 169
DB 118 -----SGDYDMFAVYGQGLTVYSAAKTTAPSVYPLAPVCGGTSSVTLGCLVAG 169
OY 176 YRPEPVYVWSGALTSVHTFPRAVLAQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHPN 235
DB 176 YRPEPVYVWSGALTSVHTFPRAVLAQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHPN 235
OY 170 YRPEPVYVWSGALTSVHTFPRAVLAQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHPN 228
DB 170 YRPEPVYVWSGALTSVHTFPRAVLAQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHPN 228
OY 236 TAYDKRVEPK-----SCDKTHCPGPCAPPELLGSPVFLPPKPPDMLISTPSPVTO 289
DB 236 TAYDKRVEPK-----SCDKTHCPGPCAPPELLGSPVFLPPKPPDMLISTPSPVTO 289
OY 229 TAYDKRVEPK-----SCDKTHCPGPCAPPELLGSPVFLPPKPPDMLISTPSPVTO 288
DB 229 TAYDKRVEPK-----SCDKTHCPGPCAPPELLGSPVFLPPKPPDMLISTPSPVTO 288
OY 290 VVDVSHEDPEVAFNMYVDGEVYVNAKTKPREQYNSTYRVSVLYTLQDMLNGEKYCKK 349
DB 290 VVDVSHEDPEVAFNMYVDGEVYVNAKTKPREQYNSTYRVSVLYTLQDMLNGEKYCKK 349
OY 289 VVDVSHEDPEVAFNMYVDGEVYVNAKTKPREQYNSTYRVSVLYTLQDMLNGEKYCKK 348
DB 289 VVDVSHEDPEVAFNMYVDGEVYVNAKTKPREQYNSTYRVSVLYTLQDMLNGEKYCKK 348

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OY 350 VSNKALPAPIEKTISKAKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEKE 409
DB 349 VNNRALPSPIEKTISKAKGQPREPOVYTLPPSRREEMTKKEKSLTCLMITEFLPAELAVDW 408
OY 410 SNGCRPNKTKTPPVYLDGSGFFLYSKLTVDSRMQGVNVCSSVNHLELHHYQKSL 469
DB 409 SNGCRPNKTKTPPVYLDGSGFFLYSKLTVDSRMQGVNVCSSVNHLELHHYQKSL 468
OY 470 LSPGK 474
DB 469 RSLGK 473

RESULT 9
OY 099LC4 PRELIMINARY; PRT; 463 AA.
AC 099LC4:
ID 099LC4:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: BC003435; AAH03435.1;
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96446; Igh-4.
DR InterPro: IPR007110; Igh-4Ike.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_v.
DR Pfam: PF00047; Iq; 4.
DR SMART: SM00406; Iq; 1.
DR PROSITE: PS50835; Iq_LIKE; 4.
DR PROSITE: PS00290; Iq_MHC; 1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 59.5%; Score 1495.5; DB 11; Length 463;
Best Local Similarity 57.6%; Pred. No. 6.6e-115;
Matches 274; Conservative 85; Mismatches 102; Indels 15; Gaps 5;

OY 1 MEGGLSMFLVAILKGVOCVOLLSSGGGLVPGGSLRLSCAASGFTFSNYAMSWYRQAP 60
DB 1 MEMWFLFLISGTAGVHSVVOLOQSGAELARPGASVRLCKASGTFYTGVSWKORT 60
OY 61 GGLGVNSAISAAGSTYLAADVSKGRFTISRDNSKNTLYIQMNSLRADFTAVYYCAKDE 120
DB 61 GGLGVNSAISAAGSTYLAADVSKGRFTISRDNSKNTLYIQMNSLRADFTAVYYCAKDE 120
OY 121 VMIIVVLNGGPDYMGCGTRVYSSASTKGPSPFLAPSSRSTSGTALGCLVYDFP 180
DB 121 VMIIVVLNGGPDYMGCGTRVYSSASTKGPSPFLAPSSRSTSGTALGCLVYDFP 180
OY 122 YSYDL-----FAVWGGLTVYSAAKTTTPPSVYPLAPGSAQTNSMTVLCGLVGFPEP 175
DB 122 YSYDL-----FAVWGGLTVYSAAKTTTPPSVYPLAPGSAQTNSMTVLCGLVGFPEP 175
OY 181 VVWSNMGALTSVHTFPRAVLAQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHPN 240
DB 181 VVWSNMGALTSVHTFPRAVLAQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHPN 240
OY 176 VVYVWNSGSLSSGVHTFPRAVLAQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHPN 234
DB 176 VVYVWNSGSLSSGVHTFPRAVLAQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHPN 234
OY 241 RVEPKSCDTHCP--CPAPPELLGSPVFLPPKPKDPMISRPPEVTCVVDVSHEDP 298
DB 241 RVEPKSCDTHCP--CPAPPELLGSPVFLPPKPKDPMISRPPEVTCVVDVSHEDP 298
OY 235 KIVPRDCG---CKPICIVPEV---SVFIFPPKPKDVIITLTPFKVCVVDISKDDP 287
DB 235 KIVPRDCG---CKPICIVPEV---SVFIFPPKPKDVIITLTPFKVCVVDISKDDP 287
OY 299 EYKFNMYVDGEVYVNAKTKPREQYNSTYRVSVLYTLQDMLNGEKYCKSKNALPAP 358
DB 299 EYKFNMYVDGEVYVNAKTKPREQYNSTYRVSVLYTLQDMLNGEKYCKSKNALPAP 358
OY 288 EYQFVSFVVDVEVHTAQTQPREQYNSTYRVSVLYTLQDMLNGEKYCKSKNALPAP 347
DB 288 EYQFVSFVVDVEVHTAQTQPREQYNSTYRVSVLYTLQDMLNGEKYCKSKNALPAP 347
OY 359 IEKTSKAGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEKESNGQENNY 418
DB 359 IEKTSKAGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEKESNGQENNY 418

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Db 348 IEKISTKGRPKAPQVYTIPTPPKEQMAKVSLTCTMTDFPEDITVEMQMGOPAPENY 407
Qy 419 KTEPVLDSDGSFFLYSKLTVDKSRMOQGNFSCSVHMEALHNHYTOKSLSPGK 474
Db 408 KNTQPIMDTDSGYFIYSKLTNOKSMWENAGNFTCSVLHGLHNHTTKSLSHSPGK 463

RESULT 10
ID 099L31 PRELIMINARY; PRT; 468 AA.
AC 099L31:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC003878; AA03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig_1Ike.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 58.6%; Score 1474; DB 11; Length 468;
Best Local Similarity 59.2%; Pred. No. 4e-113;
Matches 280; Conservative 68; Mismatches 113; Indels 12; Gaps 5;

Qy 6 SWL--FLVALIKGVOCEVQLLESGLVOPGSLRLSCAASGFTFSNYAMSVRQAPGK 63
Db 4 SMVLEFLMAVYIGVNSEVQLQSGAELVRPGASVKLSTAGSPFNKIDSLMHMVQRPGQ 63
Qy 64 LEWVSATISAGSHSTYLDASVKGRTISNDKSNKNTLYLQMSNLRAEDTAIVYICANDREYTM 123
Db 64 LEWIGWIDPEDEGRTKVPKFDKATITADTSSNTAYIQLSSLTSEDTAIYICARN----- 118
Qy 124 IVNLGDFYMGQGTTRVTVSSASTKGPVSFPLAPSSKTSSTGTAALGCLVADYPEPYTV 183
Db 119 -LLGGLYDYGQGTITTVSSAKTTAPSVYPLAPVCGDTTSSVTLGCLVAGTFPEPYTL 177
Qy 184 SWNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQYICNVNHRKPSNTKVDKVE 243
Db 178 TWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTPSSQITCNVAPASTVDKKEIE 236
Qy 244 PKSCDKHTHTCP--CPAPELLGSPSVLFPPKPKDMLISTRTPEYTCYVVDVSHEDPEVK 301
Db 237 PRG-PTIKPCPPCKCPAPNLLIGSPSVLFPKIKDVLMSLSPMYTCVVDVSEDDPVQ 295
Qy 302 FNNYVDGVEVNAKTRPREQYNSTYRVSVLYTLHODMLNGKEKCKVSKALPAPLER 361
Db 296 ISWVNVNVEVLTATQTHREDYNSTLRVVSALPIOHODMMSGKEKCKVSKALPAPLER 355
Qy 362 TISAKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEMESNQGENYKTT 421
Db 356 TISKPGSVRAPOYVLPPEPEEMTKKQVTLTCVTDMPEDIVEMTNKKTLENTYKNT 415
Qy 422 PPIVDSGGSFLLYLDKSRMOQGNVFCSVHMEALHNHYTOKSLSPGK 474
Db 416 EPVLDSDGSYFMYSKLTVEKKMVERNSYSCSVYHGLHNHTTKSFSRTPGK 468

RESULT 11
099L25

ID 099L25 PRELIMINARY; PRT; 473 AA.
AC 099L25:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC003888; AA03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig_1Ike.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE989B7986DA155 CRC64;

Query Match 57.5%; Score 1446.5; DB 11; Length 473;
Best Local Similarity 56.4%; Pred. No. 7.5e-111;
Matches 274; Conservative 75; Mismatches 112; Indels 25; Gaps 5;

Qy 1 MEFGSLWFLVALIKGVOCEVQLLESGLVOPGSLRLSCAASGFTFSNYAMSVRQAP 60
Db 1 MEMSWVLEFLFSLVTTGVSQVQLQSDALELVKPGASVKSCKVGYFTDHTIMVQRP 60
Qy 61 GKGLEWVAISAGSHSTYLDASVKGRTISNDKSNKNTLYLQMSNLRAEDTAIVYICANDRE 120
Db 61 EGLEWVIGYIYTPROGSTYNEKEFKGATLTADKSSSTAYVQMLNLSLSDSVVCFCSR--- 117
Qy 121 VTMTVLNGG-----FDYMGQGTTRVTVSSASTKGPVSFPLAPSSKTSSTGTAALG 170
Db 118 -----GGSIIYGYGLYFDYMGQGTITTVSSAKTTAPSVYPLAPVCGDTTSSVTLG 169
Qy 171 CLVNDYFPEPYTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQYICNVN 230
Db 170 CLVKGYPPEPYTVLWNSSLSGVSHTFPAVLQSD-LYTLSSSVTVTSSTPSSQITCNVA 228
Qy 231 HKPSNTKVDKREKSCDKHTHTCP--CPAPELLGSPSVLFPPKPKDMLISTRTPEYTC 288
Db 229 HPASTKYDKKIERRG-PTIKPCPPCKCPAPNLLIGSPSVLFPKIKDVLMSLSPMYTC 287
Qy 289 VVDVSHEDPEVKENWYVDGVEVNAKTRPREQYNSTYRVSVLYTLHODMLNGKEYKC 348
Db 288 VVDVSEDDPVQISMVFNNEVLTATQTHREDYNSTLRVVSALPIOHODMMSGKEKCK 347
Qy 349 KVSNAKLPAPLEKTIISAKKQPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEM 408
Db 348 KVNNAKLPAPLEKTIISKRGSVRAPOYVLPPEPEEMTKKQVTLTCVTDMPEDIVEM 407
Qy 409 ESNQGENYKTTPEPVLDSDGSFFLYSKLTVDKSRMOQGNFSCSVHMEALHNHYTOKSL 468
Db 408 TNKQTELTNTPEPVLDSDGSYFMYSKLTVEKKMVERNSYSCSVYHGLHNHTTKSF 467
Qy 469 SLSPGK 474
Db 468 SRTPGK 473

RESULT 12
08R3H6
ID 08R3H6 PRELIMINARY; PRT; 474 AA.
AC 08R3H6:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)


```
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AF212774; AK58686.1; -
DR HSSP: P00761; IAN1
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR007110; Iq-like.
DR InterPro: IPR003597; Iq-cl.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00047; Iq; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBILOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM0069; GLA; 1.
DR SMART: SM00407; IGC1; 1.
DR SMART: SM00020; TRYP_SPEC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATON; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992P CRC64;
SQ

Query Match 50.0%; Score 1257; DB 4; Length 701;
Best Local Similarity 99.1%; Pred. No. 5.7e-95;
Matches 230; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 243 EPKSCDKHTHTCPKPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 302
DB 470 EPKSCDKHTHTCPKPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 529
QY 303 NMVYDGVNHNAAKTRPREQYNSTYRVYSLTVLHODMLNGKEYCKCKVSNKALPAPIEKT 362
DB 530 NMVYDGVNHNAAKTRPREQYNSTYRVYSLTVLHODMLNGKEYCKCKVSNKALPAPIEKT 589
QY 363 ISKAKGPREPOVYTLPPSREEMTKNOVSLCLVKGFPSPDIAYEWESNGPENNYKTPP 422
DB 590 ISKAKGPREPOVYTLPPSREEMTKNOVSLCLVKGFPSPDIAYEWESNGPENNYKTPP 649
QY 423 PVLDSGSEFLYSLKLYDKSRMOQGNVSCSVMEHALNHNHTOKSLSLSPGK 474
DB 650 PVLDSGSEFLYSLKLYDKSRMOQGNVSCSVMEHALNHNHTOKSLSLSPGK 701

RESULT 15
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

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RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE-B-cell;
RA Strausberg R.;
DR EMBL: BC015760; AAH15760.1; -
DR InterPro: IPR007110; Iq-like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq-v.
DR Pfam: PF00047; Iq; 5.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263DP CRC64;

Query Match 42.2%; Score 1061.5; DB 4; Length 597;
Best Local Similarity 40.5%; Pred. No. 6.1e-79;
Matches 240; Conservative 73; Mismatches 147; Indels 133; Gaps 17;

QY 1 MEFGLSWFLVAIIKGVQCEVQLLESGGGLVQPGSLRLSCAASGFPFSNYAMSWRQAP 60
DB 1 MEFGLSWFLVAIIKGVQCEVQLLESGGGLVQPGSLRLSCAASGFSFSSYAMMMWRQAP 60
QY 61 GKGLEWVSAISASGHSTYLADEVKGRFTISRDNSKNTLYIQMNSLRADETAVYYCAND-- 118
DB 61 GKGLEWVSAISGSGSTYLADEVKGRFTISRDNSRDITLYQMNSLRADETAVYYCANDPR 120
QY 119 -----REVTVIIVLNGCFDYWGQSTRVTVSASIKGKGVPLAPSSKSTSG-GTAA 168
DB 121 GYSASGNYTR-----DYGQDTLVTVSSGSASAPTLPLVSCENSPDTSVA 169
QY 169 LGCLVKDYFPEPVTVSW--NSGALTSGVTHFPAVLQSSGLTSLSSVTPVSSSL--GTQT 224
DB 170 VGCLAQDFLPDSTIFPSMKYKKNNSDISTRGPPSVLR-GGKYAAISQVILPESKDVWGQIDE 228
QY 225 Y-ICNVNHPSPN-----TKVDKRVPEKS-----CDKHTCP-- 254
DB 229 HVCVKVQHPRNGNKKENKVPDLPVIAELPRKVSFVFPDPDFGPNPKSKLICQATGTFSPRQI 288
QY 255 -----PCPAPELLGGPS----- 266
DB 289 QVSWLRGSKQVGSVTTDQVOAEAKESGPTYYKVTSTLTIKESDMLSOSMFTCVNDRGL 348
QY 267 -----VFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVD 307
DB 349 TFGQNASMCVPDDDTAIRVFAIRPS-FASIFLTKSRKTLCTLVLDLTYYD-SVITSMTRQ 406
QY 308 GVEVHNAAKTRPREQYNSTYRVYSLTVLHODMLNGKEYCKCKVSNKALPAPIETISKAK 367
DB 407 NGEAVKHTNTISESPNPATFSAVGEASICEDDMNSGERFTCTVTHNTDLPPLKQITSRPK 466
QY 368 GQP-REPOVYTLPPSREEMT-KNOVSLCLVKGFPSPDIAYEWESNGOP--ENNYKTPP 423
DB 467 GVALHRPDVYTLPPAREDLNRESATITCLVTGFSPADVFYQMMQKGPULSPPEKYYVSAP 526
QY 424 VLD--SDGSEFLYSLKLYDKSRMOQGNVSCSVMEHALNHNHTOKSLSLSPGK 474
DB 527 MPEQARERGFYAHSLITLVSEEMNTGELTYCVVAHEALPNKVTERTYDKSKGK 579
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Search completed: September 12, 2003, 13:03:27
Job time : 85.3475 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:47:03 ; Search time 20.0847 Seconds

(without alignments)
1109.830 Million cell updates/sec

Title: US-09-848-832-3

Perfect score: 2514

Sequence: 1 MEEGLSWLFLVAILKGYQE.....MHEALHNHYTKSLSLSPGK 474

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	1758	69.9	330	1	GC1_HUMAN
2	1610	64.0	326	1	P01857 homo sapien
3	1599.5	63.6	327	1	GC4_HUMAN
4	1231.5	49.0	323	1	GC_RABIT
5	1210.5	48.2	329	1	GC2_CAVPO
6	1162	46.2	290	1	GC3_HUMAN
7	1155	45.9	326	1	GC1_RAT
8	1150	45.7	329	1	GC3_MOUSE
9	1145	45.5	324	1	GC1_MOUSE
10	1144.5	45.5	333	1	GC8_RAT
11	1140	45.3	393	1	GC1M_MOUSE
12	1139	45.3	398	1	GC3M_MOUSE
13	1129	44.9	330	1	GC4A_MOUSE
14	1127.5	44.8	329	1	GC2_RAT
15	1126.5	44.8	335	1	GCAB_MOUSE
16	1124	44.7	399	1	GCAM_MOUSE
17	1115	44.4	322	1	GC4_RAT
18	1085	43.2	336	1	GC8_MOUSE
19	1080	43.0	405	1	GCBM_MOUSE
20	577	23.0	117	1	HV3C_HUMAN
21	515.5	20.5	116	1	HV05_CARAU
22	486.5	19.4	429	1	EPIC_RAT
23	486	19.3	428	1	EPIC_HUMAN
24	485.5	19.3	136	1	HV16_MOUSE
25	479.5	19.1	122	1	HV3G_HUMAN
26	471	18.7	421	1	EPIC_MOUSE
27	466	18.5	117	1	HV54_MOUSE
28	461	18.3	117	1	HV55_MOUSE
29	460	18.3	121	1	HV3J_HUMAN
30	459	18.3	114	1	HV29_MOUSE
31	454	18.1	147	1	HV59_MOUSE
32	454	18.1	142	1	HV01_RAT
33	452	18.0	455	1	MUC_MOUSE

34	450.5	17.9	458	1	MUC_RABIT
35	450	17.9	117	1	HV58_MOUSE
36	449	17.9	115	1	HV3D_HUMAN
37	445	17.7	454	1	MUC_HUMAN
38	444	17.7	119	1	HV3I_HUMAN
39	443.5	17.6	122	1	HV3H_HUMAN
40	442	17.6	476	1	MUCM_MOUSE
41	441	17.5	117	1	HV53_MOUSE
42	440.5	17.5	479	1	MUCM_RABIT
43	440	17.5	115	1	HV3F_HUMAN
44	438.5	17.4	114	1	HV3B_HUMAN
45	437.5	17.4	126	1	HV3K_HUMAN

ALIGNMENTS

RESULT 1

ID	GC1_HUMAN	STANDARD:	PRT:	330 AA.
AC	P01857	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig gamma-1 chain C region.			
CN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrate; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RN	Biochemistry 9:3161-3170(1970).			
RP	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RT	Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RN	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RP	Biochemistry 9:3171-3181(1970).			
RP	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Postingsl H., Hilschmann N.;			
RT	"The role of antibody structure. The primary structure of a			
RL	monoclonal IgG1 immunoglobulin (myeloma protein N.e). III. The			
RP	chymotryptic peptides of the H-chain, alignment of the tryptic			
RT	peptides and discussion of the complete structure.";			
RL	Hoppe-seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RP	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884944;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RP	Hoppe-seyler's Z. Physiol. Chem. 364:713-747(1983).			
RP	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE-77070267; PubMed-1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT 19g1 immunoglobulin (myeloma protein Nle), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE-61208100; PubMed-7235608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
CC MARKER & THE GIM (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35, 116, 198, 269 & 272
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 153, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198, 267&272.
CC -----
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CC -----
DR EMBL; J00228; AAC82527.1; ALT_INT.
DR PIR; A93433; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR PDB; 1A07; 12-NOV-97.
DR PDB; 1D5B; 09-FEB-00.
DR PDB; 1D5I; 09-FEB-00.
DR PDB; 1D6V; 04-OCT-00.
DR PDB; 1DN2; 17-MAY-00.
DR PDB; 1E4K; 06-JUN-01.
DR PDB; 1FCG; 20-JUL-95.
DR PDB; 1H2H; 12-JUN-02.
DR PDB; 1H7H; 08-AUG-01.
DR PDB; 1I1S; 16-MAY-01.
DR PDB; 1I1X; 16-MAY-01.
DR PDB; 1L6X; 10-APR-02.
DR PDB; 2RC5; 12-NOV-97.
DR Genew; HGNC:5525; IGHG1.
DR MIM; 147100; .
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding activity; TAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Igcl; 2.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330 CH3.
FT DISULFID 27 83 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT VARIANT 241 241
FT STRAND 122 126
FT HELIX 130 134
FT HELIX 136 137
FT STRAND 141 147
FT STRAND 157 162
FT TURN 163 164
FT STRAND 165 166
FT TURN 168 171
FT STRAND 176 179
FT TURN 180 181
FT STRAND 182 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 209 210
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
FT STRAND 245 256
FT STRAND 260 265
FT STRAND 270 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 305 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 325
SQ SEQUENCE 330 AA; 36106 MM; 3770EE106C2FA33D CRC64;
Query Match 69.9%; Score 1756; DB 1; Length 330;
Best Local Similarity 99.1%; Pred. No. 1.5e-113;
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 145 ASTKGPSVFPLAPSSKSTSGTALAAGLVADYDPPEPTVAMNSGALTSGVHTTPAVYLQSS 204
DB 1 ASTKGPSVFPLAPSSKSTSGTALAAGLVADYDPPEPTVAMNSGALTSGVHTTPAVYLQSS 60
QY 205 GLVSLSSVIVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTPCPPAPPELLGG 264
DB 61 GLVSLSSVIVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTPCPPAPPELLGG 120
QY 265 PSYFLPPPKPKDGLTMTISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPREQYN 324
DB 121 PSYFLPPPKPKDGLTMTISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPREQYN 180
QY 325 STYRVSVLVTLVLQDMLNGKEYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSRREE 384
DB 181 STYRVSVLVTLVLQDMLNGKEYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSRREE 240
QY 385 MTRKQVSLTCLVKGFPYSDIAYVESNGOPENNKTTPPYLDSGSEFYLTKLTVDSRW 444
DB 241 LTRKQVSLTCLVKGFPYSDIAYVESNGOPENNKTTPPYLDSGSEFYLTKLTVDSRW 300

QY 445 OQGNVSCSVMEALHNHYTKSLSPGK 474
 DB 301 OQGNVSCSVMEALHNHYTKSLSPGK 330

RESULT 2
 GC2_HUMAN STANDARD: PRT: 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RX TISSUE=Fetal liver;
 RA MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 evolution of a gene family.";
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RX TISSUE=Fetal liver;
 RA MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbits T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes.";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stopnini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";

RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 CC -----
 DR EMBL: J00230; AAB59393.1; .
 DR PIR: A93906; G2HU.
 DR HSSP: P01857; 1RC1.
 DR GeneW: HGNC:5526; IGHG2.
 DR MIM: 147110; .
 DR GO: GO:0005624; C:membrane fraction; NAS.
 DR GO: GO:0003823; F:antigen binding activity; TAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR003597; Ig-like.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; IGc1; 2.
 DR PROSITE: PS00835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109 C->S (IN REF. 3).
 FT SEQUENCE 326 AA; 35884 MW; 831087BC687BCF9C CRC64;
 SQ

Query Match 64.0%; Score 1610; DB 1; Length 326;
 Best Local Similarity 91.8%; Pred. No. 2e-103;
 Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 145 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNNGALTSGVHFPFVAVLOSS 204
 DB 1 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNNGALTSGVHFPFVAVLOSS 60

QY 205 GLYSLSSVYTVPSNFGTQTYICNVNHRPSNKKVKKRPPKSCDCTHCPAPAPELGCG 264
 DB 61 GLYSLSSVYTVPSNFGTQTYICNVNHRPSNKKVKKRPPKSCDCTHCPAPAPELGCG 116

QY 265 PSVFLEPPKPKDITLISRTPEVTCVAVVDVSHEDPVKKFMVYDVGVEVHNAKRPPEDEQYN 324
 DB 117 PSVFLEPPKPKDITLISRTPEVTCVAVVDVSHEDPVKKFMVYDVGVEVHNAKRPPEDEQYN 176

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QY 325 STYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 384
  117 STYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 236
QY 385 MTKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 444
  237 MTKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 296
QY 445 QCGNVFSCSVMEALHNHYTKSLSPGK 474
  297 QCGNVFSCSVMEALHNHYTKSLSPGK 326
Db

RESULT 3
GC4_HUMAN STANDARD; PRT: 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DY 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
GN Ig gamma-4 chain C region.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=63157104; PubMed=6299662;
RX Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP MEDLINE=70207560; PubMed=4192699;
RX Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
  Blochem. J. 117:33-47(1970).
RL
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CC -----
DR EMBL: K01316; AAB59394.1; ALT_INIT.
DR PIR: A90933; GAHU.
DR PDB: IADQ: 16-SEP-98.
DR GeneW: HGNC:5528; IGHG4.
DR MIM: 147130.
DR GO: GO:0005624; C:membrane fraction; NAS.
DR GO: GO:0003823; F:antigen binding activity; TAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS00835; IG_LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT DOMAIN 1 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

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FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 63.68; Score 1599.5; DB 1; Length 327;
Best Local Similarly 91.88; Pred. No. 1.1e-102;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 145 ASTKGPSVFLPAPSAKSTSGTAALGCLVDFYPPETPTVMSNGALTSVHTPAAVLQSS 204
  1 ASTKGPSVFLPAPSAKSTSGTAALGCLVDFYPPETPTVMSNGALTSVHTPAAVLQSS 60
Db
QY 205 GLYSLSVTVTPSSSLGTQTYICNVNHRPSNTRVDRKVERPKSCDKHTTCCPPAPRLGG 264
  61 GLYSLSVTVTPSSSLGTQTYICNVNHRPSNTRVDRKVERPKSCDKHTTCCPPAPRLGG 117
Db
QY 265 PSVFLPPEPKKDTLMISRTPEVTCVVYVDSHEDPEVKFNNYVDGVEVHNAKTKPREQYN 324
  118 PSVFLPPEPKKDTLMISRTPEVTCVVYVDSHEDPEVKFNNYVDGVEVHNAKTKPREQYN 177
Db
QY 325 STYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 384
  178 STYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 237
Db
QY 385 MTKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 444
  238 MTKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 297
Db
QY 445 QCGNVFSCSVMEALHNHYTKSLSPGK 474
  298 QCGNVFSCSVMEALHNHYTKSLSPGK 327
Db

RESULT 4
GC_RABIT STANDARD; PRT: 323 AA.
ID GC_RABIT
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DY 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
GN Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP MEDLINE=64030930; PubMed=6313520;
RX Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
  F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP MEDLINE=76135469; PubMed=1243651;
RX Pratt D.M., Moie L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
  immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP MEDLINE=83299917; PubMed=6193512;
RX Martens C.L., Moore K.W., Steilmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
  heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP MEDLINE=70110015; PubMed=5461106;
RX Fruchter R.G., Jackson S.A., Moie L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
  immunoglobulin G.";

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RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Ledovitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (in) Kiliander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 Stockholm (1967).
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
 CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 CC MARKERS AND REF.5 THE E15 MARKER.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
 CC -----
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 CC -----
 CC EMBL: M16426; AAA31289.1; -
 DR PIR: A91749; GHRB.
 DR HSSP: P01857; IEC1.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 RV Immunoglobulin domain; Immunoglobulin C region; Repeat.
 FT NON_TER 1
 FT DOMAIN 1
 FT 6 96 IG-LIKE 1.
 FT 114 213 IG-LIKE 2.
 FT DOMAIN 2
 FT 222 318 IG-LIKE 3.
 FT VARIANT 104 104 T->M (IN D11 MARKER).
 FT 185 185 T->A (IN E15 MARKER).
 FT CONFLICT 48 48 N->E (IN REF. 2).
 FT 71 71 V->VPY (IN REF. 2).
 FT CONFLICT 144 144 Q->E (IN REF. 3 AND 4).
 FT 173 173 Q->D (IN REF. 5).
 FT CONFLICT 187 187 Q->E (IN REF. 3 AND 5).
 FT CONFLICT 201 201 N->D (IN REF. 5).
 FT CONFLICT 218 218 Q->E (IN REF. 5).
 FT CONFLICT 233 233 E->Q (IN REF. 5).
 FT CONFLICT 246 246 N->D (IN REF. 5).
 FT CONFLICT 256 256 E->G (IN REF. 5).
 FT CONFLICT 260 260 N->D (IN REF. 5).
 FT CONFLICT 266 266 N->D (IN REF. 5).
 FT CONFLICT 280 280 Y->W (IN REF. 5).
 FT CONFLICT 284 284 N->S (IN REF. 5).
 SO SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 49.0%; Score 1231.5; DB 1; Length 323;
 Best Local Similarity 70.0%; Pred. No.1-8e-77;
 Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 148 KGPSVFPLAPSSKSTSGGTAALGLCLVLYKDYFPEPVTVSNVSGALTSGLVHTFPAVLQSSGLY 207
 Db 4 KAPSVFPLAPCCGDPSPSTVTLGCLVKGYLPEPVTVVNSGTLTGVRFPFVSQGLY 63
 QY 208 SLSSVYVYVSSSLGTQYICVANKRPSKTKYDKRREPSCDKTHTCCPCPAPELLGGSYV 267
 Db 64 SLSSVSVYVSSS---QPVTCVAVHATNTKVKDYTPAFTCSK---PTCPPELILGGSV 116
 QY 268 FLFPPPKDPTLMISRTPEVTCVAVDVSHDEPEVKRNMVVDGVEVNAKTKEPDEQNGSY 327
 Db 117 FIFPPKRDITLMISRTPEVTCVAVDVSDDEPVQDTWIMNNEQVYTAHPPLREQDFNSTI 176
 QY 328 RVSVSVLVVADHWLNGKREYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTK 387
 Db 177 RVSVSTLPITTHQDWLRGKFEKCKVHNKALPAPIEKTISKARQGLEPQVYTYGMPREDELSS 236

QY 388 NOVSLTCLYKGFPSDIAVEMESNGCPENNYKTPPEVLDSD3SFLYSLKLVYDKSRMOG 447
 Db 237 RVSLSLTCHINGFPYSPDISVEMKNGKAEDNTTTRAVLDSD3SYFLINKLSVPTSEMRG 296
 QY 448 NVFSCSVMEALHNHYTKSLSPGK 474
 Db 297 DVFTCSVMHEALHNHYTKSLSPGK 323

RESULT 5
 GC2_CAVPO
 ID GC2_CAVPO STANDARD; PRT; 329 AA.
 AC P01862;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-2 chain C region.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OX NCBI_Taxid=10141;
 RN [1]
 RA Trischmann T.M.;
 RL Submitted (Apr-1975) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 4-68.
 RX MEDLINE=71058471; PubMed=5538606;
 RA Birstein B.K., Hussain Q.Z., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). 3. Amino acid sequence of the
 RT half-cysteine joining heavy and light chains.";
 RL Biochemistry 10:18-25(1971).
 RN [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RX MEDLINE=71058486; PubMed=5538616;
 RA Turner K.J., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT and hinge region cyanogen bromide fragments.";
 RL Biochemistry 10:9-17(1971).
 RN [4]
 RP SEQUENCE OF 134-226.
 RX MEDLINE=75036072; PubMed=4429665;
 RA Tracey D.E., Cebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4796-4803(1974).
 RN [5]
 RP SEQUENCE OF 227-311.
 RX MEDLINE=75036073; PubMed=4609467;
 RA Trischmann T.M., Cebra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4804-4811(1974).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71058474; PubMed=4922544;
 RA Oliveira B., Lamm M.E.;
 RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
 RL Biochemistry 10:26-31(1971).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
 CC 13 INBRED GUINEA PIGS.
 CC PIR: A94553; G2GP.
 DR HSSP: P01842; 7FAB.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 RV Immunoglobulin domain; Immunoglobulin C region; (i)ycoprotein.

FT	VARIANT	126	127		OY -> EA (IN ZUC).
FT	VARIANT	134	134		/FTID=VAR_003890.
FT	VARIANT	139	139		P -> L (IN OMM).
FT	VARIANT	182	182		/FTID=VAR_003891.
FT	VARIANT	182	182		F -> Y (IN OMM).
FT	VARIANT	227	227		/FTID=VAR_003892.
FT	VARIANT	227	227		T -> A (IN OMM).
FT	VARIANT	227	227		/FTID=VAR_003893.
FT	VARIANT	227	227		S -> N (IN OMM).
FT	VARIANT	227	227		/FTID=VAR_003894.
FT	VARIANT	279	279		MISSING (IN ZUC).
FT	VARIANT	279	279		/FTID=VAR_003895.
FT	VARIANT	279	279		E -> Y (IN OMM).
SO	SEQUENCE	290 AA;	32331 MM;	E69CBBC95705B2F46 CRC64;	
<hr/>					
Query Match					
Best Local Similarity 46.2%; Score 1162; DB 1; Length 290;					
Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0					
<hr/>					
OY	EPKSCDKTHTPCPPAPPELLGSPVFLTPPKPDTLMSRTPEVCVVVDVSHEDPEVKF	302			
Db	59 EPKSCDPRPCRCRAPPELLGGPSVFLTRPKKDTLMISRTPEVCVVVDVSHEDPEVQF	118			
OY	303 NMVYDGVEVNAKTARKPREOYNSTYRVVSVLTVLHODMLNGEKYCKYSNKALPAPIEKT	362			
Db	119 KMYVDGVYVNAKTARKPREOGFNSTFRVSVYLTVLHQNMLDGEKYCKYSNKALPAPIEKT	178			
OY	363 ISKAKGQPREOVYTLTPRSREEMTKNQVSLTCLVKGFITPSDIAVWESNGQPENNYKTTP	422			
Db	179 ISKRGQGREPOVYTLTPRSREEMTKNQVSLTCLVKGFYPSDIAVWESSGOENNNTTP	238			
OY	423 PVLDSGDSFFLYSKLTVDKSRMWOEGSNVSCVMHEALTNHYTOKSLSPGK	474			
Db	239 PMLDSDGSFFLYSKLTVDKSRMQGNITRSCVMHEALTNRFTQKSLSPGK	230			
<hr/>					
RESULT 7					
ID	GCL_RAT	STANDARD:	PRT:	326 AA.	
AC	P20759:				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig gamma-1 chain C region.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_taxid=10116;				
RP	SEQUENCE FROM N.A.				
RX	BREDLINE=89232738; PubMed=3149946;				
RA	Brieglebmann M.,				
RT	"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";				
RL	Gene 74:473-482(1988).				
DR	PIR: PS0017; PS0017.				
DR	HSSP: POI842; 7FAB.				
DR	InterPro: IPR007110; Ig-like.				
DR	InterPro: IPR003597; Ig-cl.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	Pfam: PF00047; Ig_3.				
DR	SMART: SMO0407; IGc1_2.				
DR	PROSITE: PS00835; IG_LIKE; 3.				
KW	PROSITE: PS00290; IG_MHC; 1.				
FT	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.				
FT	NON_TER	1			
FT	DOMAIN	1	97		CH1.
FT	DOMAIN	98	112		HINGE.
FT	DOMAIN	113	219		CH2.
FT	DOMAIN	220	326		CH3.
FT	DISULFID	27	82		
FT	DISULFID	102	102		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	106	106		INTERCHAIN (WITH A HEAVY CHAIN).

FT	DISULFID	109	109	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	111	111	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	140	200	
FT	DISULFID	146	304	
FT	CARBOHYD	176	176	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	326 AA;	35946 MW;	013BAB455EF49B9DA C1C64;
Query Match				
Best Local Similarity		45.9%;	Score 1155;	DB 1; length 326;
Matches 211;		Conservative 52;	Pred. No. 3,2e-72;	Mismatches 60; Indels 10; Gaps 4;
QY	145	ASTGCPSPYFLAPBSKSTSGCTAALGCLVRYKFFPEPPTVYSINSGALISGVTFFPAVLQSS	204	
DB	1	AETTPASPYPLAPBPSTALKSNMWTGLCLVKCYFPPEPTVTVINSGLISGVTFFPAVLQ-S	59	
QY	205	GLYLSLSSVWTPSSSLGQTYICNVHNPSTXKDKRKREPI:SCCKTHICPCPAPELLGG	264	
DB	60	GLYTVLSSVTVPSSTWSPSQVYTCNVANHPASTKDKKTVLPINCG--GDCKKCC---ICTG	113	
QY	265	--PSVLEFPKPKDPTLMSRTPEVTCVVDVSHEDBEVKINMYVDGEVHNATKPRE	321	
DB	114	SEVSVSVFLEPPKPRDVLITLTPKVTQVVDISQDDPEVHI:SWFVDDVEVHTAQTRPEE	173	
QY	322	QYNSTYRVVSVLTVLHODMLNGKCKCKSVSKALPAPIEK:ISAKGQPREPOVYTLPPS	381	
DB	174	QFNSTFRVSSELPIHDMDLNGFRFCRVTSAAPEPIEK:ISKPEGRTOVPHYVTMSPT	233	
QY	382	REEMTKNOVSLTCLVKGFPSPDIADVEMSNCPDENNKTTI:PVLDSSQSFYLSKLTVDK	441	
DB	234	KEEMTKNEVSLTICVWKGFPDIDVEMSNCPDENNKNTI:PTMDTDSYFLSKLVNKK	293	
QY	442	SRMOQGVNFCSCVNHREALNNHYTKOISLSPGK	474	
DB	294	EKMQGNFTFCSVLHEGLHNNHTKESLSHSBGK	326	
RESULT 8				
GC3_MOUSE				
ID	GC3_MOUSE	STANDARD:	PRT:	329 AA.
AC	P22436:			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-3 chain C region, secreted form.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrati; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85027161; PubMed=6092053;			
RA	Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,			
RA	Tucker P.W., Blattner F.R.;			
RT	"Structural analysis of the murine IgG3 constant region gene";			
RL	EMBO J. 3:2041-2046(1984).			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation --			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL, J00451. -, NOT_ANNOTATED_CDS.			
DR	PIR, B02156; G3MSC.			
DR	HSSP, P01857; IFC1.			
DR	InterPro: IPR007110; Ig-like.			
DR	InterPro: IPR003597; Ig_c1.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig_3.			
DR	SMART, SM00407; Igcl. 2.			
DR	PROSITE, PS50835; Ig_LIKE. 3.			

DR PROSITE: PS00290; IG_MHC.1
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;
 Query Match 45.7%; Score 1150; DB 1; Length 329;
 Best Local Similarity 65.0%; Pred. No. 76-72;
 Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;
 QY 146 STKGSPVPLAPSSKSTSGGTALCLVKDYPEPEVTVSMNSGALTSGVHTPPAVLQSSG 205
 DB 1 TTTAPSVYPLVPGCGDSTGSSVTLGLCVKGYGPEPEVTVSMNSGALTSGVHTSSVLQ -SG 59
 QY 206 LYSLSVTVPPSSSLGTOTYTCNVNHNKPSNTKVDRKVEPKSCDKTHITCP-FCPAPELLG 263
 DB 60 FYSLSLVTPSPSTPSPQVTCNVNHNKPSNTKVDRKVEPKSCDKTHITCP-FCPAPELLG 118
 QY 264 GPSVPLFPKPKDMLISRTPEVTVSMNSGALTSGVHTPPAVLQSSG 323
 DB 119 GPSVPLFPKPKDMLISRTPEVTVSMNSGALTSGVHTPPAVLQSSG 178
 QY 324 NSTVSVSVLYLVLDHDLNGKRYKCKVSKKALPADIETKSKAKQPREPVYTLPPSRE 383
 DB 179 NSTFVSVSALPIQHDMMKRGKCKVNNKALPADIETKSKAKQPREPVYTLPPSRE 238
 QY 384 EMTKQVSLTCLVKRFPSPDIAVEMESNGQPENNKTPPVLDSDGSPFLYKLVNDSKR 443
 DB 239 QMSKKKVLTLCTVTFESEAISVEBERNGELEQDYKNTPIIDSDGTYFLSKLVVDSD 298
 QY 444 WOQGVFSCSVMEALHNHYTKSLSLSPGK 474
 DB 299 WLQGEIFTCVYHEALHNHYTKSLSLSPGK 329
 RESULT 9
 GCL_MOUSE STANDARD: PRT; 324 AA.
 AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-1 chain C region secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Horjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=80202559; PubMed=6769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
 cloned in a bacterial plasmid.";
 RL Gene 9:87-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=8001837; PubMed=113776;
 RA Rogers J., Clarke P., Salsler W.;
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
 heavy chain.";

RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=78242288; PubMed=98524;
 RA Adetungbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 murine myeloma gamma1 chain.";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Secreted;
 CC IsoId=P01868-1; Sequence=Displayed;
 CC Note=May be the major isoform;
 CC Name=Membrane-bound;
 CC IsoId=P01869-1; Sequence=External;
 CC -----
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 CC -----
 DR EMBL: V00793; CAA24172.1; -
 DR EMBL: V00793; CAA24173.1; -
 DR EMBL: V00793; CAA24174.1; -
 DR EMBL: V00793; CAA24175.1; -
 DR EMBL: V00793; CAA24176.1; -
 DR PIR: A02159; G1MS.
 DR PDB: 1IGC; 03-JUN-95.
 DR GLCOSuitedB: P01868; -
 DR MGD: MGI:96446; 1gh-4.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; 1g; 3.
 DR SMART: SM00407; IGc1; 2.
 DR PROSITE: PS00835; IG-LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174
 FT DISULFID 244 302 N-LINKED (GLCNAC. . .).
 FT MOD_RES 324 324 /FTID=CAR_000055.
 FT CONFLICT 276 276 REMOVED POST-TRANSLATIONALLY.
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3DIFZC93 CRC64;
 Query Match 45.5%; Score 1145; DB 1; Length 324;
 Best Local Similarity 62.3%; Pred. No. 15e-71;
 Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
 QY 145 ASTKGSPVPLAPSSKSTSGGTALCLVKDYPEPEVTVSMNSGALTSGVHTPPAVLQSS 204

[illegible][illegible]

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CC -----
DR EMBL: V00793; CAA24172.1; -
DR EMBL: V00793; CAA24173.1; -
DR EMBL: V00793; CAA24174.1; -
DR PIR: B02159; G1MSM.
DR PDB: 1SC8; 23-MAR-99.
DR PDB: 1AE6; 18-MAR-98.
DR PDB: 1CL7; 12-JAN-00.
DR PDB: 1F11; 06-FEB-01.
DR PDB: 1F58; 29-DEC-99.
DR PDB: 1KCS; 24-JUL-02.
DR PDB: 1KCR; 11-MAY-02.
DR PDB: 25C8; 09-JUL-99.
DR MGD: MGI:96446; Igh-4.
DR Interpro: IPR007110; Ig-like.
DR Interpro: IPR003597; Ig-cl.
DR Interpro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00407; IGc1; 2.
DR PROSITE: PS50835; IG_LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane; 3D-structure.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFD 27 82
FT DISULFD 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFD 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 138 198 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHD 174 174 N-LINKED (GLCNAC. . .).
FT TRANSME 244 357
FT TRANSME 340 357 POTENTIAL.
FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7ALCE27 CRC64;

Query Match 45.3%; Score 1140; DB 1; Length 393;
Best Local Similarity 62.2%; Pred. No. 4.3e-71;
Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;

OY 145 ASTGSPVPLAPSSKSGGALGCLVKDYFPEPVVSWNSGALTSGVHPFPAVLQSS 204
DB 1 AKTTPPSVPLAPSAAGTSMKVTGLCKGTFPEPVVWNSSGSLGSHVFPVAVLQSD 60
OY 205 GLYSLSSVTVPLPSSSLGTQTYICNVNHRPSMTKVKVREPKSCDTHHCPR--CAPELL 262
DB 61 LYTSSSVTVPLPSSSRPESETVTCNVNHRPASSTKVKTIYPRCC---CKPEICIVPEV- 114
OY 263 GGPVSEVLPKPKDTLMSIKRPEVTCVVDVSHDEPVKFMVYVDGVEVHNKTRPREQ 322
DB 115 --SSVFIPPKPKDILTITLPKVCVVDVSKDDEVOFSFVVDVEVHFGQTPREBO 172
OY 323 YNSGTVRVSVLTVLHODMLNGKEYCKVSKNAKLPRIKTIKSKAGQREPOVYTLPSR 382
DB 173 FNSFTRSVSELPIMHODMLNGKEFGCRVNSAFAFPARIKTIKSKGRKAPQVYTIIPPK 232
OY 383 EEMKRNQVSLTCLVGYFPDIAVEMSGNPENNYKTPPLVLDGSGFFSLTKLVKS 442
DB 233 EQMAKDKVSLTCLMITDFEPEDITYEMQNGQPAEKYKTKQTPIMNTNGSFYSLKLVKS 292
OY 443 RMQGGNVFSSVMHEALHNHYTKSLSPG 473

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DB 293 NMEAGNTFCSVLHGLHNHHTKSLSPG 323
: |||:|||||:|||||:|||||
RESULT 12
GC3M_MOUSE STANDARD; PRT; 398 AA.
ID GC3M_MOUSE
AC P03987;
DT 23-OCT-1986 (rel. 02, Created)
DR 01-AUG-1991 (rel. 19, Last sequence update)
DR 15-JUL-1999 (rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMOB J. 3:2041-2046(1984).
[2]
RN SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Ketman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC -----
DR EMBL: J00451; AAB59655.1; -
DR EMBL: V01526; CAA24767.1; ALT_SEQ.
DR PIR: A02156; G3MSM.
DR HSSP: P01857; 1FC1.
DR Interpro: IPR007110; Ig-like.
DR Interpro: IPR003597; Ig-cl.
DR Interpro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00407; IGc1; 2.
DR PROSITE: PS50835; IG_LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSME 346 362
FT DOMAIN 363 398 POTENTIAL.
FT DISULFD 333 333 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 342 342 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CFF264B50A41B95 CRC64;

Query Match 45.3%; Score 1139; DB 1; Length 398;
Best Local Similarity 64.7%; Pred. No. 5.1e-71;
Matches 213; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

OY 146 STGKSPVPLAPSSKSGGALGCLVKDYFPEPVVSWNSGALTSGVHPFPAVLQSS 205
DB 1 TTTAPSVPLPVGCSDTSGSSVTLGLCKVGFPEPVVKNWNGALSSGVRTVSVLQ--SG 59

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OY 206 LYSLSVVTVPSSSLGNOFYICNVNHPSTFKVDKRVKPEKSCDKTHTCP--PCPAPELLG 263
      |||||:|||||: :||| ||| | | :|||: | | | |||
Db 60 FVSLSSLVTPSSSTWPSQYVICVAHPASTKLTLEIKLEP-IRKPTSPSSCPPGNLTG 118
OY 264 GSPVFLFPKPKDITLMSRTPEYTCVVDVSHEDPEVKFMVYDGEVHNKAKTPREEQY 323
      |||||:|||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
Db 119 GSPVFLFPKPKKALMISLPKVTGVVDVSEDDPPVHSMFVDNKNVHTAMQPRRAQY 178
OY 324 NSTIRVSVLTLYLHODMLNGKEYCKVSKALPAPLEKTSKAKGQPREPOVYTLPPSRE 363
      |||: ||| | : |||: |||: |||: |||: |||: |||: |||: |||: |||
Db 179 NSTIRVVSALPIQHOQMRKEKFCVNNKALPAPLEKTSKPKGRQPTQVYTIIPPRE 238
OY 384 EMTKNQVSLTCLVKGYPDIAVEMNSGQPENNYKTTTPVLDSDGSFFLYSKLTYDVS 443
      :||: ||||| ||| : ||| ||| ||| : ||| |||: ||||| |||
Db 239 QMSKKKVSLLTCLVTNFFSEAIISYEMERNGELDYPKNTPLDSDGYFLYSKLYVDTS 298
OY 444 WQGNVSCSVMEHALNHYTKSLSLSP 472
      | | :|||: |||||: |||: |||
Db 299 WLGELFTCSVYHEALHNHTOKNLSRSP 327

RESULT 13
GCAA_MOUSE STANDARD; PRT; 330 AA.
ID GCAA_MOUSE AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g gamma-2A chain C region, A allele.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-T., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN 12
RP SEQUENCE FROM N.A.
RA MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN 13
RP SEQUENCE FROM N.A.
RA MEDLINE=81223894; PubMed=6787604;
RA Ollio R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN 14
RP MYELOMA PROTEIN MOPC 173.
RA MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the FC fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN 15
RP DISULFIDE BONDS.
RA MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
-----

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-----
DR EMBL; V00796; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; 12-JUL-01.
DR PDB; 1E4X; 12-JUL-01.
DR PDB; 1MNU; 06-MAY-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 44.9%; Score 1129; DB 1; Length 330;
Best Local Similarity 63.9%; Pred. No. 1,9e-70;
Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;

OY 145 ASTRGSPVFLPAPSSKSTSGTALGCLVDRPEPYV;MNSGALSGVHTPPAVLQSS 204
      | | |||: ||| | : | : ||| | ||| | : ||| | ||| | ||| | ||| | |||
Db 1 AKTTAPSVYPLPAPGDTGSSVTLGCLVKGYPPEVTL;MNSGSLSSGVHTPPAVLQSD 60
OY 205 GLYSLSVTVTPSSSLGTQYICNVNHPSTFKVDKVE;KSCDKTHTCP--CPAPELL 262
      ||: ||| ||| ||| : : || | | | : ||| | ||| | ||| | ||| | |||
Db 61 -LYTSLSSVTVTSTWPSQSIITCNVAHPASTKVDKIE;RG-PTIRPCPCPCPAPNLT 118
OY 263 GSPVFLFPKPKDITLMSRTPEYTCVVDVSHEDPEVK;NMVYDGEVHNKAKTPREEQ 322
      |||||: ||| | ||| : | ||| ||| | ||| : |||: ||| | : ||| | : |
Db 119 GSPVFLFPKPKIDVLMISLPYTCVVDVSEDDPPVQISMFVNVEVHTAQTQTHRED 178
OY 323 YNSTIRVSVLTLYLHODMLNGKEYCKVSKALPAPLEKTSKAKGQPREPOVYTLPPS 362
      ||||| ||| | : |||: |||: |||: |||: |||: |||: |||: |||: |||
Db 179 YNSTIRVVSALPIQHOQMRKEKFCVNNKALPAPLEKTSKPKGRQPTQVYTIIPPRE 238
OY 383 EMTKNQVSLTCLVKGYPDIAVEMNSGQPENNYKTTTPVLDSDGSFFLYSKLTYDVS 442
      ||||| |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
Db 239 EMTKQVTLTCWTDMPEDIYEWNNKTELTNTKNTSPVLDSDGSFYMSKLVREVK 298
OY 443 WQGNVSCSVMEHALNHYTKSLSLSPGK 474
      | | :|||: |||||: |||: |||
Db 299 WVGELFTCSVYHEALHNHTKLSRTEGK 330

RESULT 14
GCC_RAT STANDARD; PRT; 329 AA.
ID GCC_RAT AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g gamma-2C chain C region.
OS Rattus norvegicus (Rat).
-----

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP MEDLINE=88166903; PubMed=3127222;
 RX Bruggemann M., Delmastro-Galile P., Walmann H., Calabi F.;
 RA "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
 RT region cDNA: extensive homology to mouse gamma 3.";
 RL Eur. J. Immunol. 18:317-319(1988).
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 CC -----
 CC EMBL, X07189; CAA30169.1; -
 DR PIR: S00847; S00847.
 DR HSSP: P01842; 7EAB.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003587; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS50835; IG-LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 97
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 222 H2.
 FT DOMAIN 223 329 CH3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 143 203
 FT DISULFID 249 307
 SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;
 Query Match 44.8%; Score 1127.5; DB 1; Length 329;
 Best Local Similarity 62.8%; Pred. No. 2.5e-70;
 Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;
 QY 145 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVYVSNMGSALITSGVHTFPVAVLOSS 204
 DB 1 AATTAPSVYPLVPGGSGTSGSLVLTGCLVKGYFPEPVYVKNMGSALSSGVHTFPVAVLO-S 59
 QY 205 GLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVKRVRPKSCDTHHCPP--CPAPRL 261
 DB 60 GLYTLSSSVYTPSSSVSSQTYICVAHNPATKSNLKRLEPR---RPKRPPLDITSCDDN 116
 QY 262 LGPSVLEFPKPKDTLMISRTPEVYCVAVVDVSHDEPEVKFNWYDGVENNAKTRPRE 321
 DB 117 LGRPVLEFPKPKDTLMISRTPEVYCVAVVDVSEEPDQVSMFVDNVAVFPAQIQPHBE 176
 QY 322 QYNSVRYVSVLTVAHOMLNKEKCKVSNKALPAPIEKTSKAKGQPREQVYTPP 381
 DB 177 QLNQFRRVSTLHIOHDMMSGKCKVKNKDLSPLEKTSKRGKARQVYTPP 236
 QY 382 REEMTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPPVLDSDGSFFLYSKLVYDK 441
 DB 237 RQEMKKNVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPPVLDSDGSFFLYSKLVYDK 296
 QY 442 SRMOGVNFSVCSVMHEALHNHYTQKSLSLSPCK 474
 DB 297 DSMRGDITVCSVMHEALHNHYTQKSLSLSPCK 329

GCAB_MOUSE
 ID GCAB_MOUSE STANDARD; PRT; 335 AA.
 AC P01864;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2A chain C region secreted form (B allele).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=82037861; PubMed=6170065;
 RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
 RT "Multiple differences between the nucleic acid sequences of the
 RT IgG2a and IgG2b alleles of the mouse."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=82037777; PubMed=6794027;
 RA Dognin M.J., Lauwereys M., Strosberg A.D.;
 RT "Multiple amino acid substitutions between murine gamma 2a heavy
 RT chain C regions of Ig1a and Ig1b allotypic forms."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name-Secreted;
 CC IsoId=P01864-1; Sequence=Displayed;
 CC Note-Probably the major isoform;
 CC Name-Membrane-bound;
 CC IsoId=P01865-1; Sequence=External;
 CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
 CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
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 CC -----
 CC EMBL, J00479; -; NOT_ANNOTATED_CDS.
 DR PIR: A02153; G2MSAB.
 DR PDB: 1B0G; 23-MAR-99.
 DR PDB: 1HH6; 26-JAN-01.
 DR PDB: 1HH9; 12-JAN-01.
 DR PDB: 1HI6; 08-FEB-01.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003587; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS50835; IG-LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
 KW 3D-structure; Repeat.
 FT NON_TER 1 98
 FT DOMAIN 1 98 IG-LIKE 1.
 FT DOMAIN 126 225 IG-LIKE 2.
 FT DOMAIN 234 330 IG-LIKE 3.
 SQ SEQUENCE 335 AA; 36596 MW; FA3382792CB13C6 CRC64;
 Query Match 44.8%; Score 1126.5; DB 1; Length 335;
 Best Local Similarity 61.6%; Pred. No. 2.9e-70;
 Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;
 QY 145 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVYVSNMGSALITSGVHTFPVAVLOSS 204
 DB 1 AATTAPSVYPLVPGGSGTSGSLVLTGCLVKGYFPEPVYVKNMGSALSSGVHTFPVAVLO-S 59

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Db      1 AKTAAPSVYPLVPVCGTGTGSSVTIGCLVKGYPPEPVTLTWNSGSLSGVHTFPALLQ-S 59
QY      205 GLYSLSSVYTPVSSSLGTOTYICNVNHRKSNTRKVDKRVPRK-----SCDKTHTCPPCA 258
        |||:||| ||| :| | ||| | :||| | :|||
Db      60 GLYTLSSSVYTVSNTPSQITICNVNHPASSSTRKVDKRIEPRVPITONPCPPHQVPVPCAA 119
        |||:||| ||| :| | ||| | :||| | :|||
QY      259 PELLGAPSVLEFPKPKDITMISRPEPVTCVVDVSHEDPEVKEFNVYDGVVEVHNAKTKP 318
        |:||| ||| ||| :| | ||| | :||| | :|||
Db      120 PLLLGPSVFIFPPKIKDYLMTISLSPMTCVVDVSEDDPDVQISNFWNNVEVHTAQOT 179
        |||:||| ||| :| | ||| | :||| | :|||
QY      319 REEQYNSTYRVVSVLTVLHQDMLNKEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 378
        | ||| ||| | : ||| :||| :||| :||| :||| :|||
Db      180 HREDYNSLTRVYSALPIQHODWMSGKEFKCKVNNRALPSPIEKTISKPRGVPVRAPOVYL 239
        |||:||| ||| :| | ||| | :||| | :|||
QY      379 PPSREEMTKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLT 438
        || |||| : |||| : ||| :||| :||| :||| :|||
Db      240 PPPAEEMTKKEFSLCMITGFLPAETIAVDMTISNGRTEONYKNATVLDSDGSYFMYSKLR 299
        || |||| : |||| : ||| :||| :||| :||| :|||
QY      439 VDKSRMOQGNVFCSVMHEDALHNHYTQKSLSLSPGK 474
        | ||| :||| :||| :||| :||| :||| :|||
Db      300 VOKSTWERSLFACSVHVEVHLNHLTKTISRSLGK 335
        || |||| :||| :||| :||| :||| :||| :|||
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